

FIG. 1

HPP-CFC (Colony #)

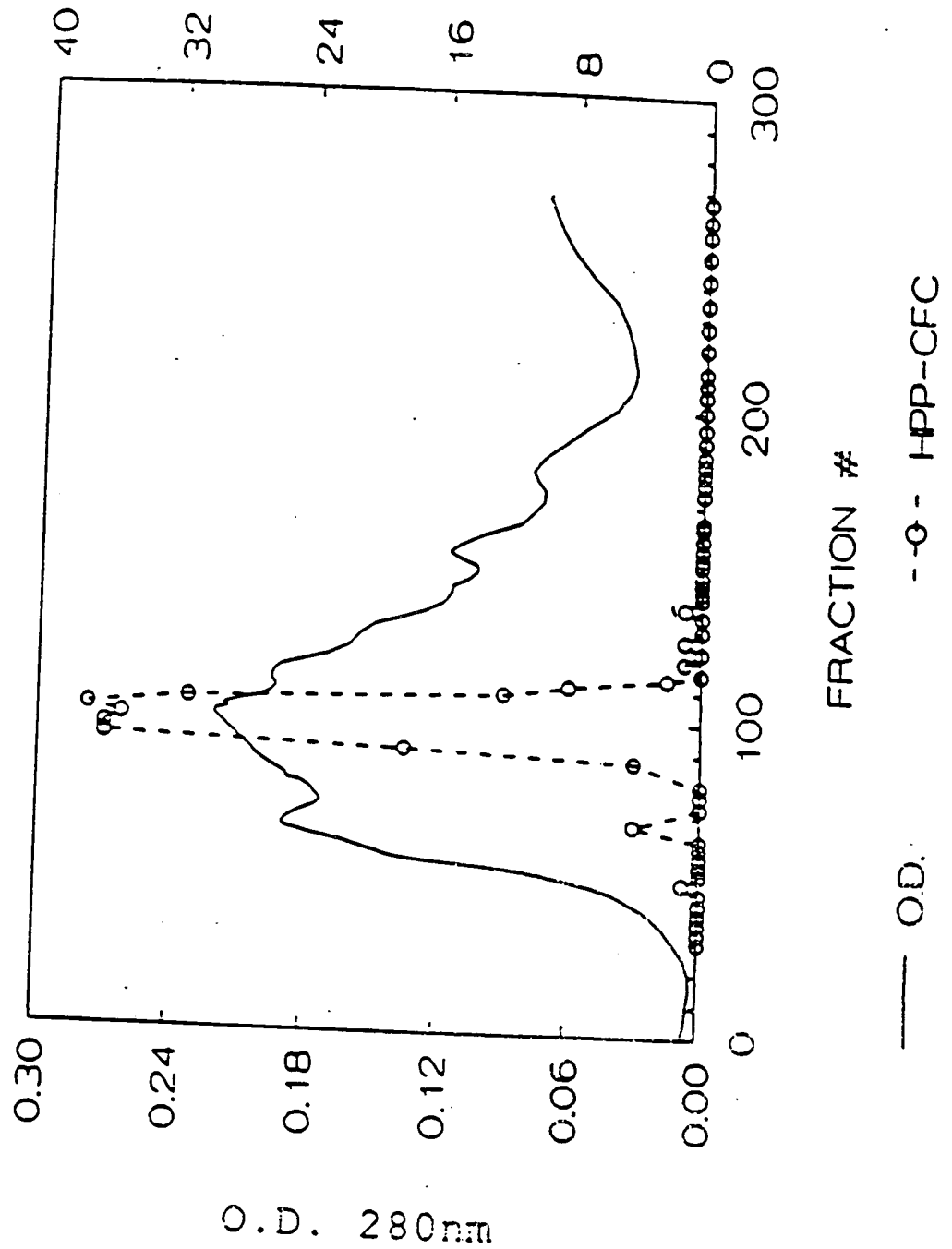


FIG. 2

HPP-CFC (Colony #)

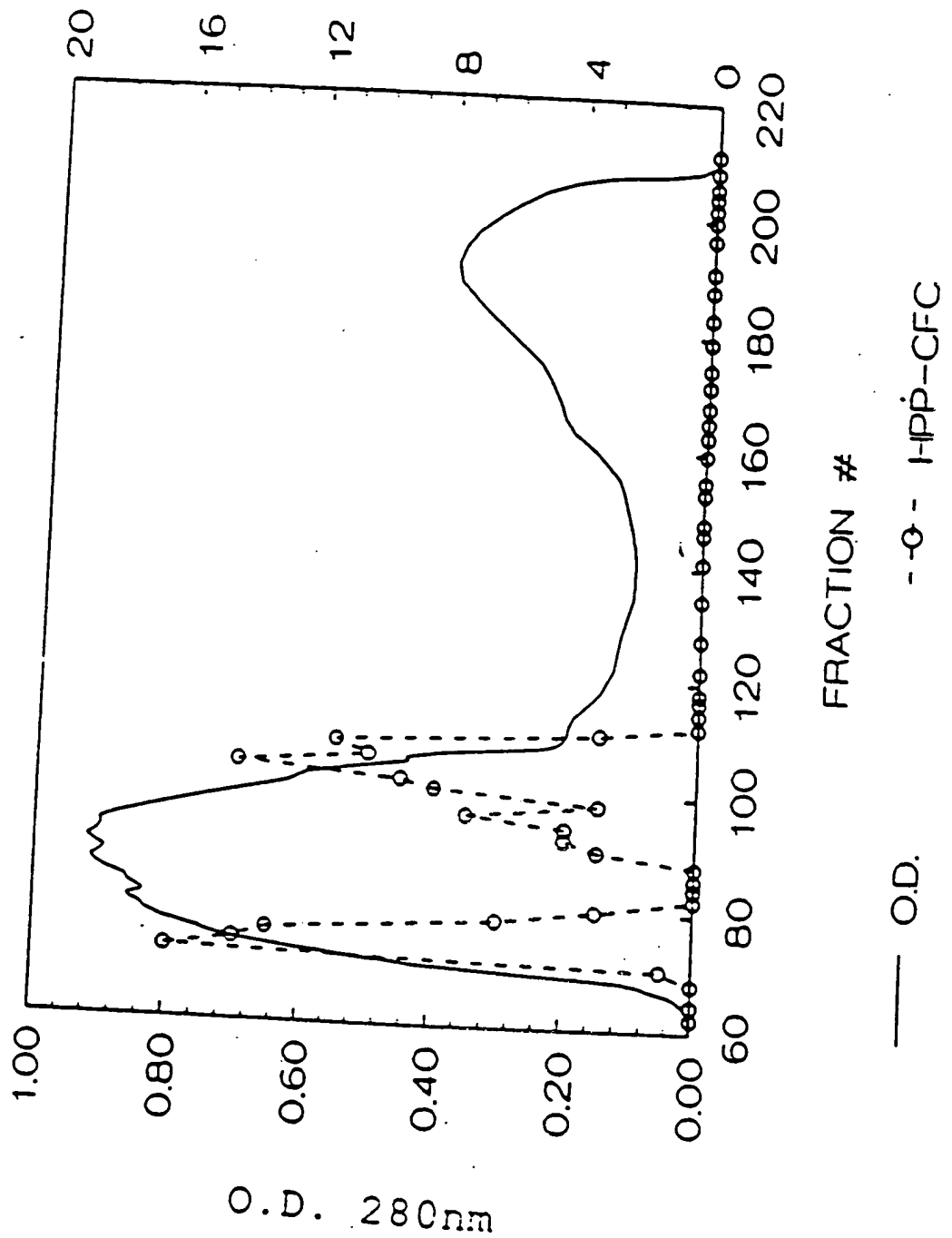


FIG. 3

MC/9 CPM (X 10⁻³) OR HPP-CFC (col. #)

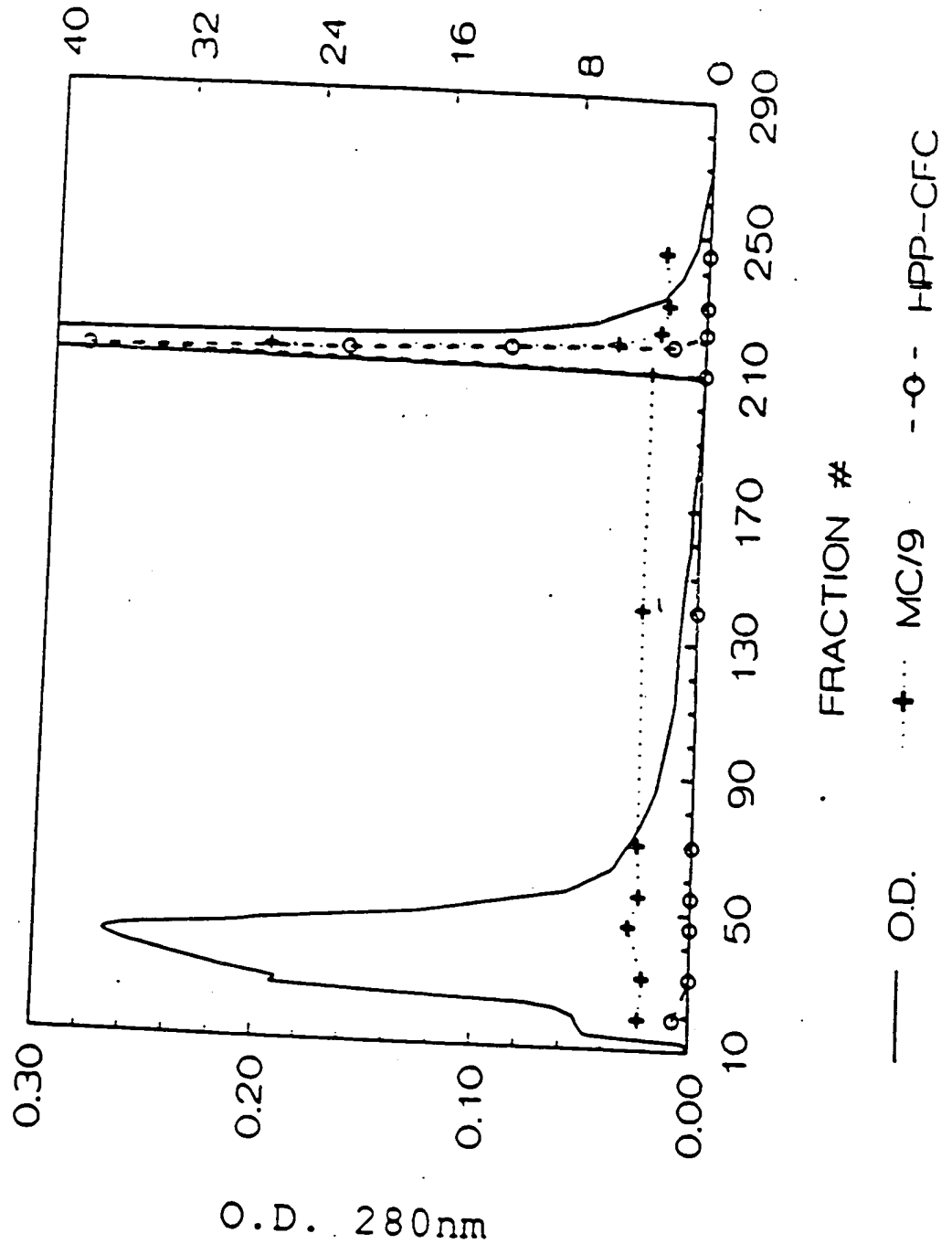


FIG. 4

MC/9 CPM ($\times 10^{-3}$)

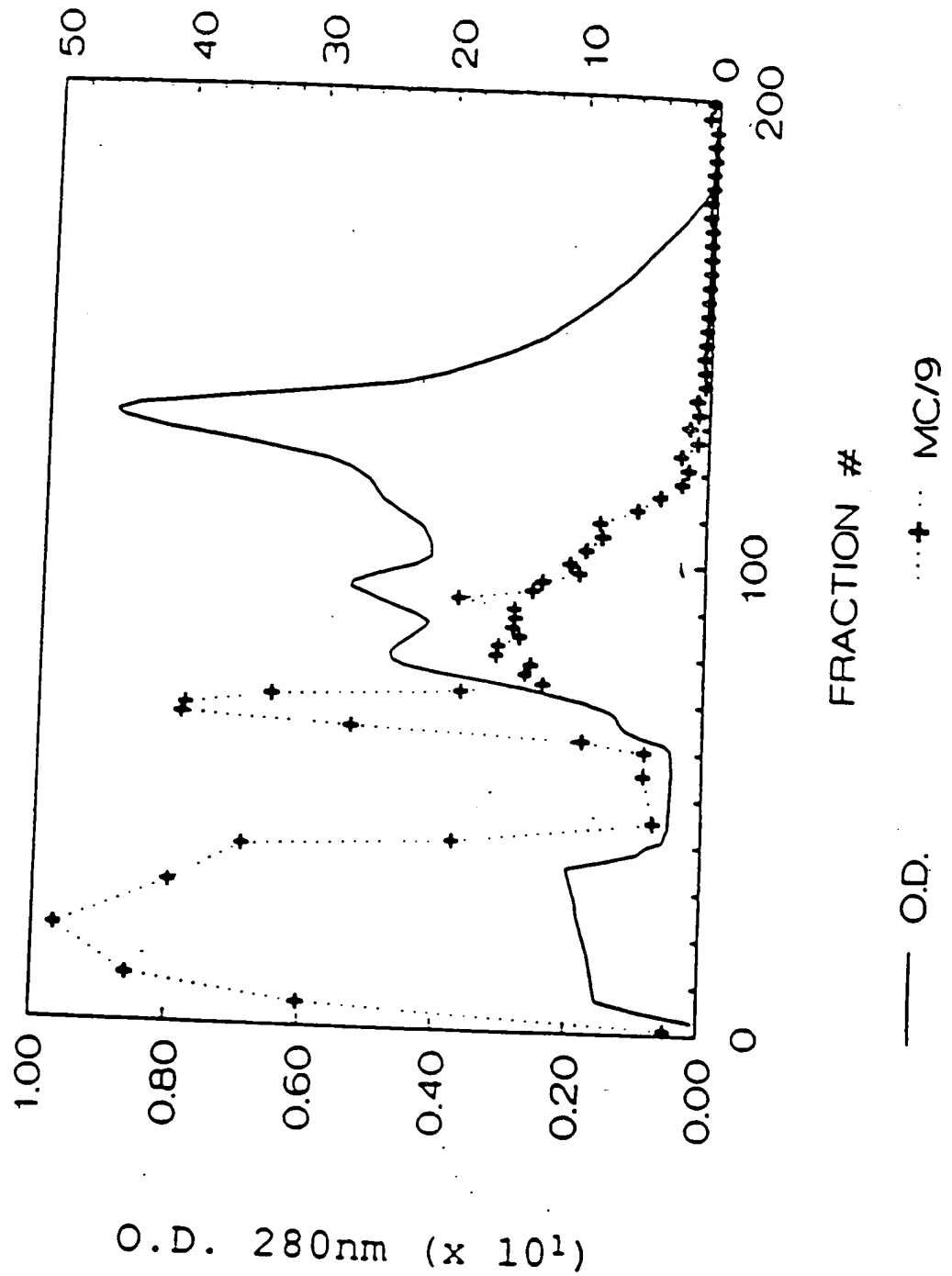


FIG. 5

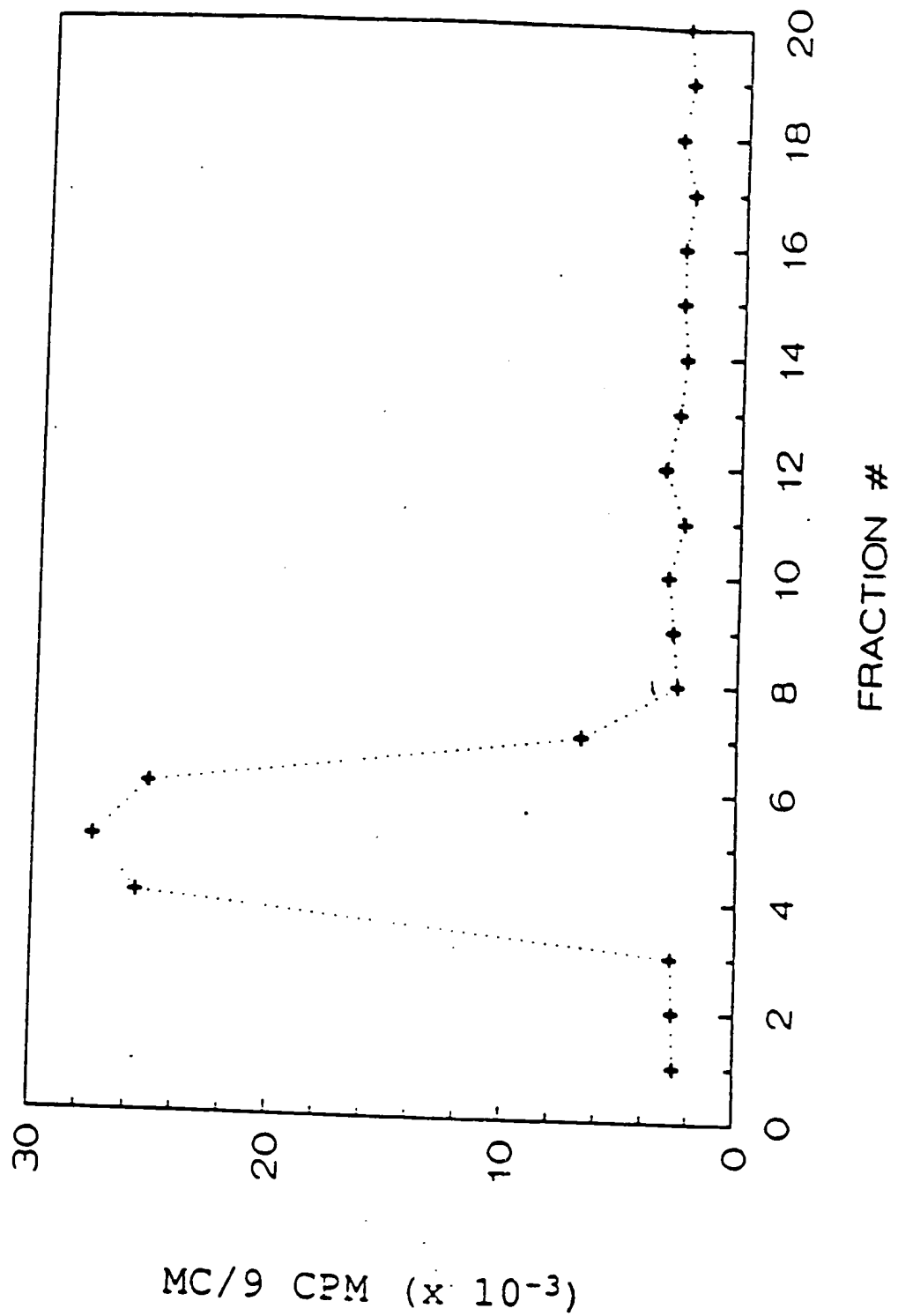


FIG. 6

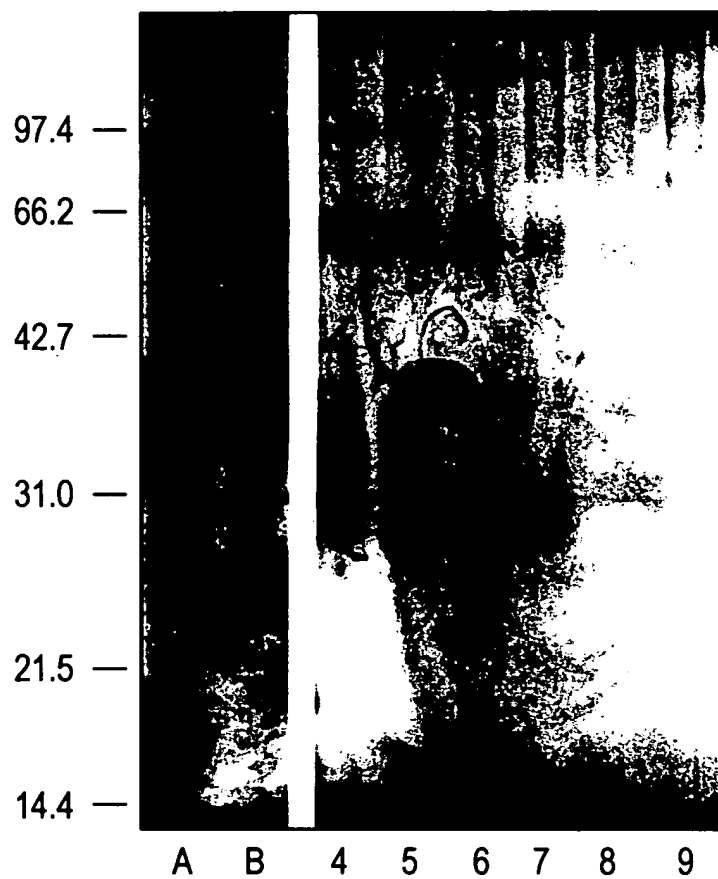


FIG. 7

MC/9 CPM

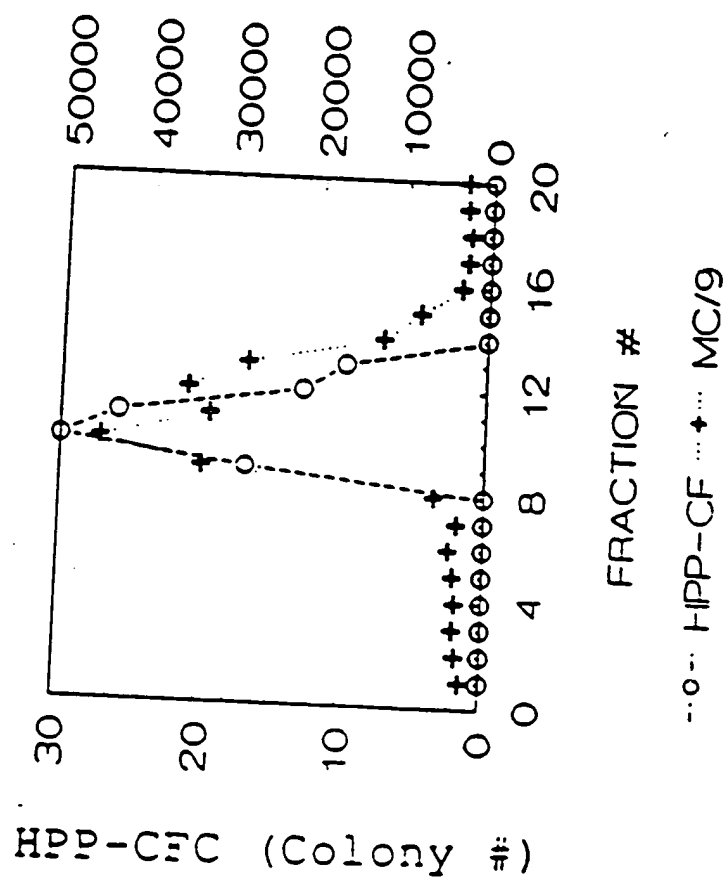


FIG. 8

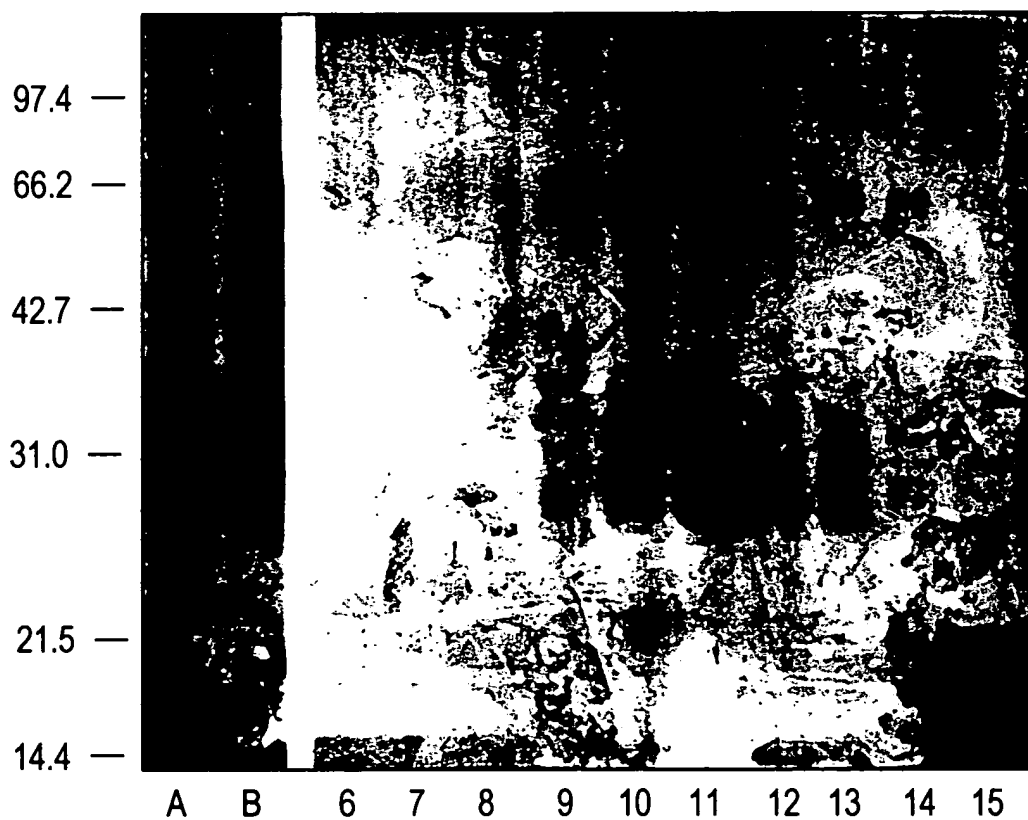


FIG. 9

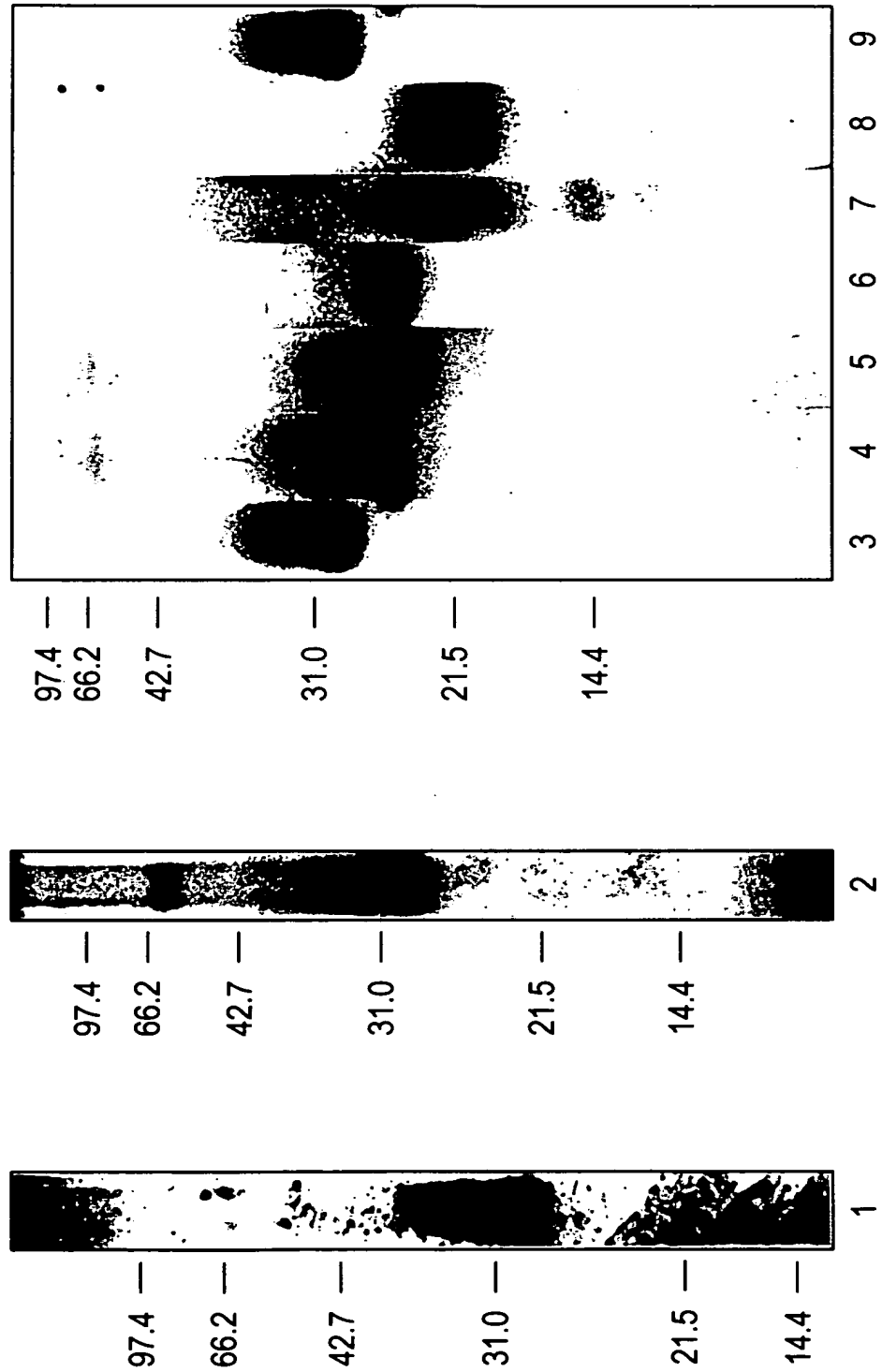


FIG. 10

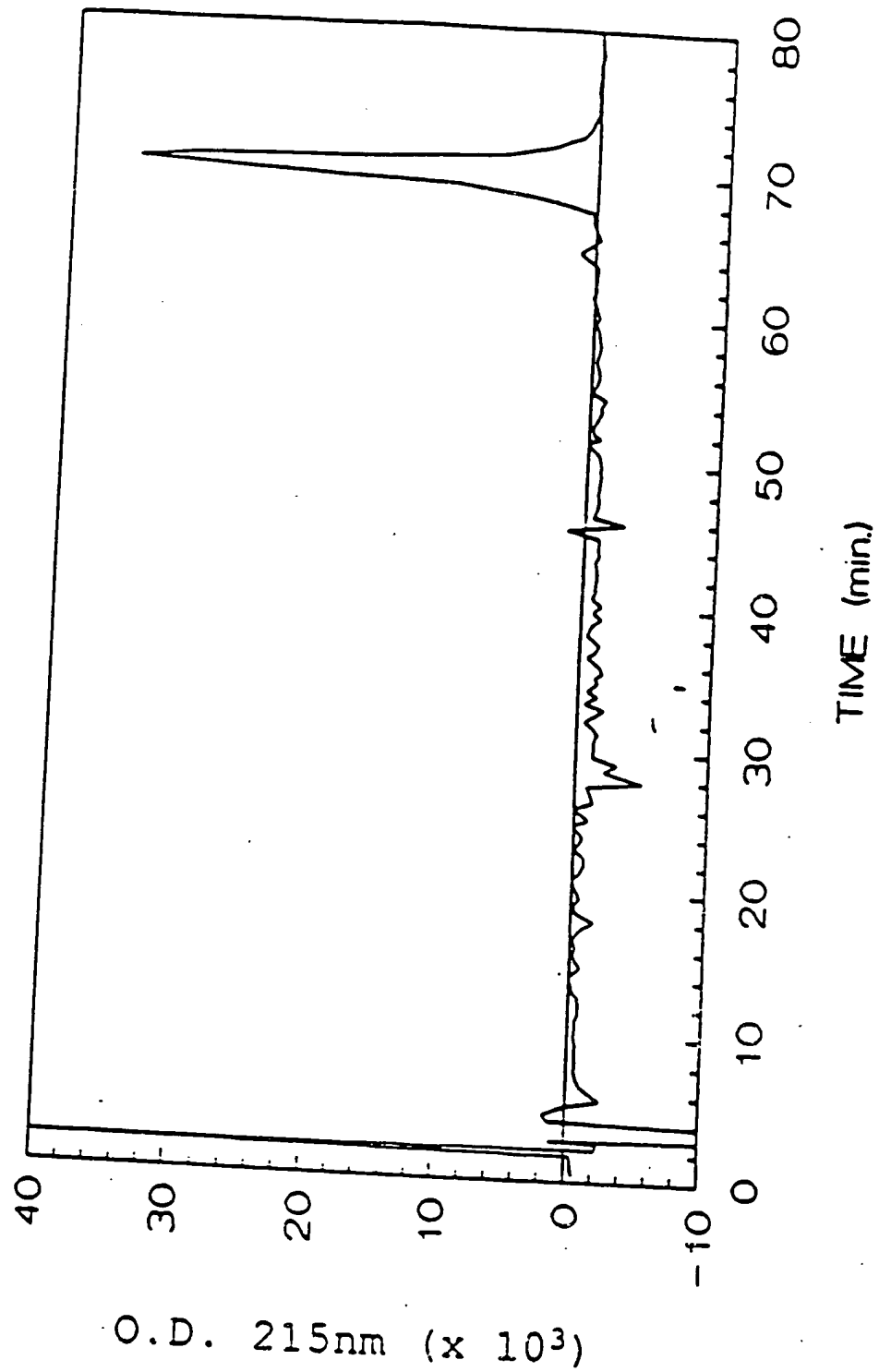


FIG. 11

1 10 20
pE E I C R N P V T D N V K D I T K L V A N L P N D
----- Sequencing after -----
----- T-5a -----
30 40 50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment ----->
----- T-5a -----
----- CB-6a ----- CB-8; CB-10 -----
60 70
H L S V S L T T L L D K F S N I S E G L S N Y S I
----- Sequencing after Trp Cleavage -----
80 90 100
I D K L G K I V D D L V A C M E E N A P K N V K E
----- T-3 -----
----- CB-14; CB-15; CB-16 -----
----- S-1 -----
110 120
S L K K P E T R N F T P E E F F S I F N R S I D A
--- T-1 ----- T-4 (N109 nonglyco) -----
----- T-7 (N120 glyco); T-8 (N109 nonglyco) -----
----- CB-14; CB-15; CB-16 -----
----- S-5 or S-6 (N109 nonglyco) -----
130 140 150
F K D F M V A S D T S D C V L S S T L G P E K D S
----- T-5b -----
----- CB-6B -----
----- S-5 or S-6 -----
160
R V S V T K P F M L P P V A(A)
----- T-2 ----- (Carboxypeptidase)
----- CB-6B -----
----- S-2 -----

FIG. 12A-1

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTIGGIGCATTCCTCCAT G T G T T	393-368
219-22	AAAACTCCTCIGGIGTAAATT G T T G G	447-425
219-25	GTTTCNGGTTTTT C C C	420-407
219-26	ATGGAAGAAACGCCCCCAAACGT G G T G T	368-393
222-11	CCNAATGATTATATGATAAC C C C C T	167-186
222-12	GGNGGNAACATAAANGGCTT G G T	566-585
223-6	ACCATAAAATCTTTAAACGATC G G C G G	492-470
224-24	GATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

FIG. 12A-2

224-28	TAACCAACAATGACTAGGCAA	235-215
225-31	TTCCAGAGTCAGTGTC	547-562
227-29	GCGAAGCTTGCCCTTCCCTTATGAAGAAGA	16-35 *
227-30	GCGCCGCGGTACGGTGGTAACATGAAGGGCTTTGTGA	586-561 *
228-30	GATAAATGCAAGTGATAATCC	45-65
230-25	GCGGTCGACCCGCGGAACCTTAAAGTCCATGCAACAC	705-685 *
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592 *
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595 *

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACCTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190

FIG. 12C

OLIGO	SEQUENCE
201-7	CCCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG. 13A

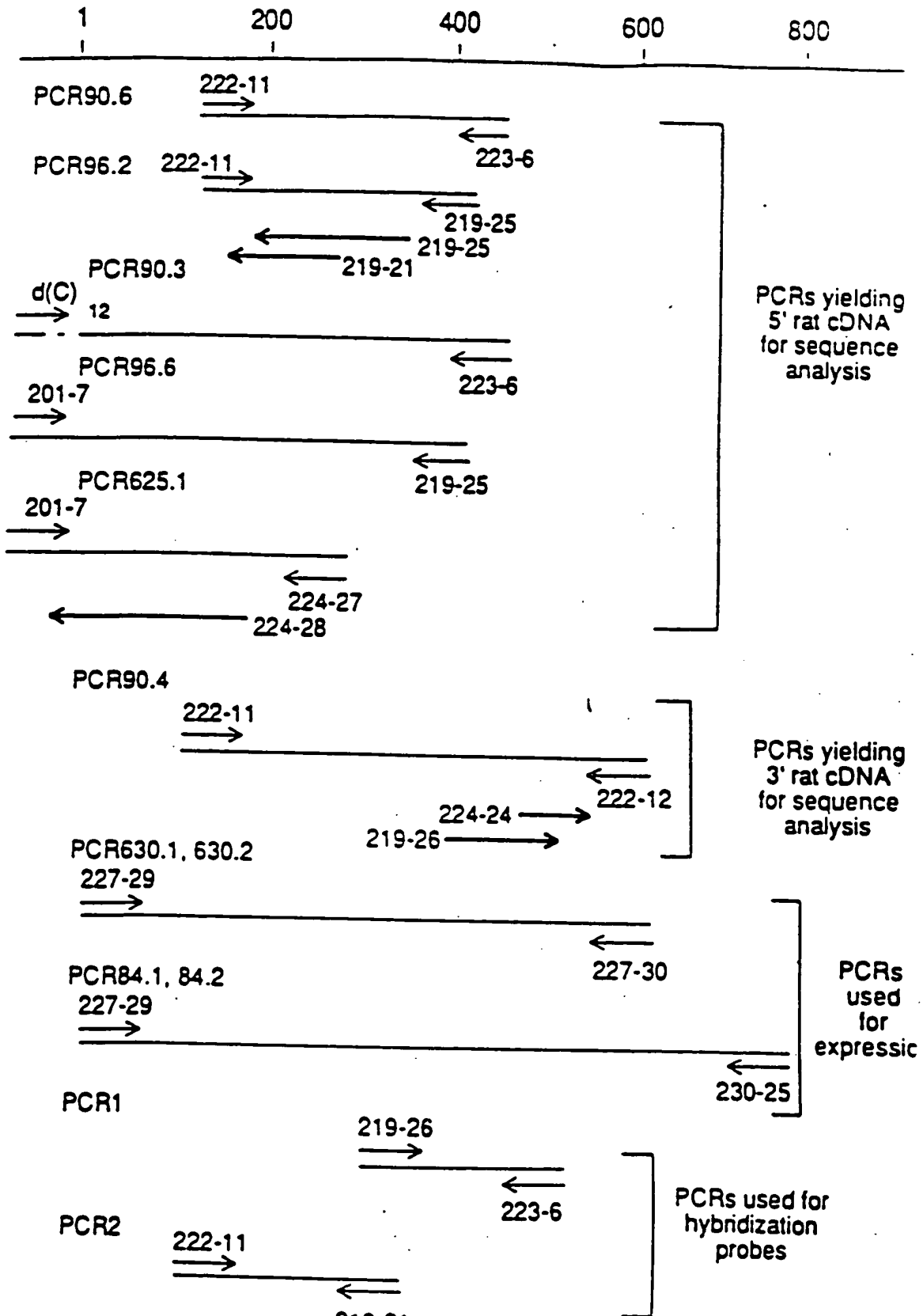


FIG. 13B

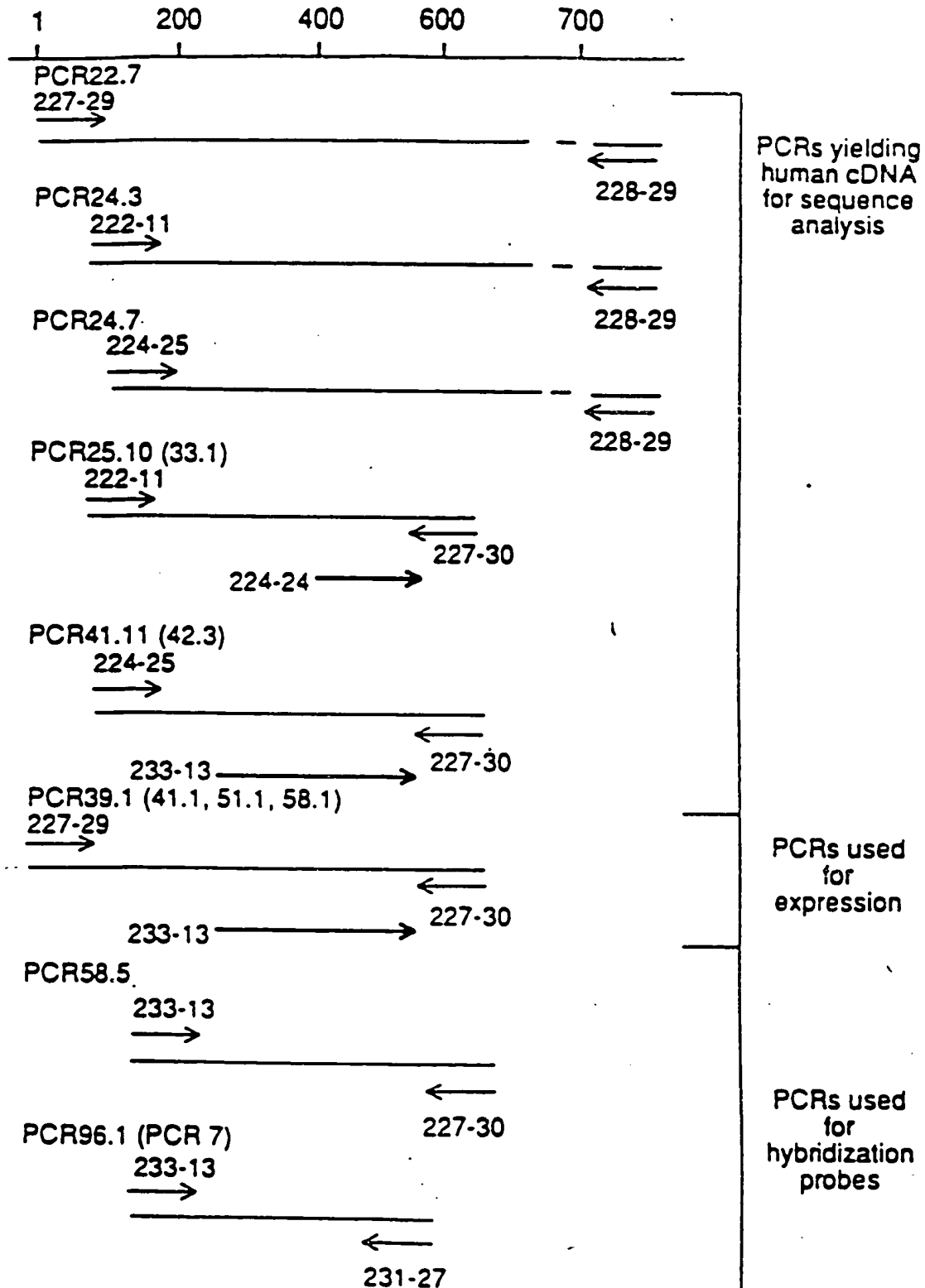


FIG. 14A

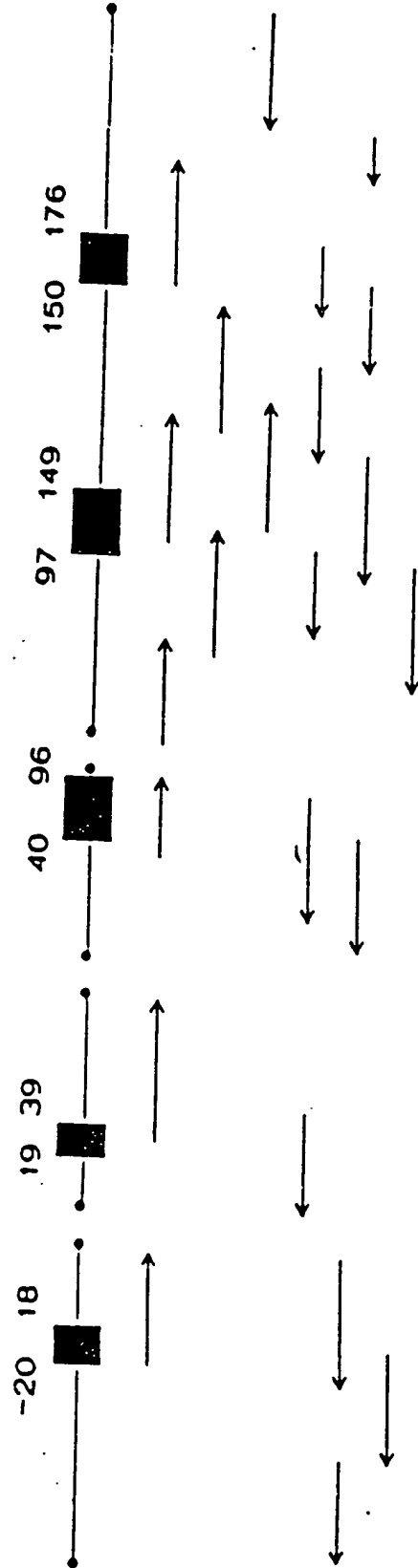


FIG.14B-1

AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT	45
AAACA _n ACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT	90
TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA	135
TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT	180
TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG	225
AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTTCATGCATTTCCT	270
CCATTTTCCGAGGTCCCcCcAAGTGATAATTCTGTTACACGTTG	315
CTACAAGTTCATCCCTAATTGCCGTCAAGAACTGACTGTAGAAG	360
GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT	405
AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC	450
TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT	495
AAGCCATCAGCTTAAACAAAACAAAACAAAACAAAAAAAACCC	540
CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC	585
TGGTTTGCATAGTTCTGGATTTTTTTTTTTTAAAACTGATGGAC	630
-20	
ThrT _r pIleIleThrC	
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT	675
-10	
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG	
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAACTC	720
1	10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT	
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA	765

FIG.14B-2

CAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC	810
CTGTGCTTGCTGACCACATAGGTTTCAGGGCACTCCCGACAGGAGT	855
TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC	900
TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC	945
TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT	990
TTGCCTGTTACCTACTG	1007

Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA	45
TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA	90
TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT	135

19

Val

TCTCTTGTATTTACTCACGTTTTTCATTTCTTGGTCTCTGTAGGTG	180
--	-----

30

AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla	
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC	225

39

GlyMetAspValLeu

GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT	270
---	-----

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT	315
---	-----

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT	360
---	-----

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT	405
---	-----

TTTCCCTACTGCTTTTAAAGCAATGGCGTCTCTTTCAGCTTCCCT	450
---	-----

FIG.14B-3

CCGATGTTAATTTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG	495
TTAAAATCATGTAAATTTCTCCTTGGCTATGTTATTTCTCATG	540
GCTATGTTATTCCTATTCGTATTTCAATTTAAAGGGACGGGAATATT	585
TATTGTATTTCTGAACTTTTTTCAGGCATGCATCCGGGTCTTTGAA	630
TAAAA	635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA	45
ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA	90
GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG	135
AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG	180
GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT	225
TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT	270
TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAACTCTTTGTCT	315
GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA	360
ATCTGCCATATTTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTC	405

40.

50

ProSerHisCysTrpLeuArgAspMetValThrHisLeu	
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA	450

60

SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer	
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT	495

70

80

GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle	
---	--

FIG.14B-4

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

90 96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585

ACTTGGTATTCATCAGAATTATTTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45
GAGGACATTATCCCCTCCTTGGATGCCATAGGAATCTGCTCTCAA 90
ATATGTAGATAACCACTCTGCCACCTCAGCACATACATACACATA 135
ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180
TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225
TTAAAGGCTAATTCTTATTTTGTAAATAAGCAGCTTTAAAATTCTT 270
AATTGTTTTTTTCGGGTCACCTTTATTGTCCTATTGCCACGACATTG 315
TCCTGTCCCATTTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360
CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405
TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTAAATT 450
ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495
AGTCAAGTCTATGAGTTATTTGAAAAC TAGAATCTTTGTTAATTA 540

97
AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100 110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

FIG.14B-5

GAATCACTGAAGAAGCCAGAACTAGAACTTTACTCCTGAAGAA 630

120

PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe
TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC 675

130 140

MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu
ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA 720

148

GlyProGluLysA
GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT 765

ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC 810

TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA 855

ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT 900

GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA 945

AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT 990

GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA 1035

AGATTTACGTCTCATGTCTTTTCCATAAGGTTCAAACCTCTGAGA 1080

CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC 1125

CCGAGCTGGGTCCCTATGGGGGAACTAACTTCATTGCTTTCTTTT 1170

AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT 1215

TCCTAAGCATGTCTGTGCATGCATAAGCCTTCACTCTACAAGAC 1260

AGTTATGGTGTATCGCTTGACAAAACCTGAGCAGCCAAGCTGAGTA 1305

TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT 1350

GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA 1395

FIG.14B-6

150
spSerArgV
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG 1440

160
alSerValThrLysProPheMetLeuProProValAlaAlaSerS
TCAGTGTCACAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT 1485

170 176
erLeuArgAsnAspSerSerSerSerAsn_
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC 1530

TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT 1575

GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG 1620

TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG 1665

TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA 1710

ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC 1755

GAAATTAATTGAAGGAAAAAAAAAATACAAGCAAGGCCTTATTTTG 1800

AATCATGGTAGGCTTAAATAGACTTTGTGGAGAATGTCCCTGAT 1845

CAAAGTGGAGTTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC 1890

AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG 1935

CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA 1980

TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT 2025

TGcCCAAGAACCCAcGTTCCCTGGAAGACTATCTTATTTTCATGTC 2070

TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT 2115

CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA 2160

AAGAAAGTTCTCTGAAGTCCATGCCTTTAGAATGTTTCTCTATCAA 2205

FIG.14B-7

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC	2250
CCTGAAAAATATATTTACAGTGTAGACATTTGATATACATCTAA	2295
GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC	2340
CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC	2385
ATGCATATAACATATCAGATCCTCGAGC	2413

FIG.14C-1

```

-25      -20
M K K T Q T W I I T C I
CTGGATCGCAGCGCTGCCTTTCCCTTATGAAGAAGACACAACTTGGATTATCACCTGCAT 60

-10      1
Y L Q L L L F N P L V K T Q E I C R N P
TTATCTTCAACTGCTCCTATTATTAATCCTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC 120

10      20
V T D N V K D I T K L V A N L P N D Y M
TGTGACTGATAATGTAAAGACATTACAAACTGGTGGCGAATCTTCCAAATGACTATAT 180

30      40
I T L N Y V A G M D V L P S H C W L R D
GATAACCCCTCAACTATGTGCGCGGATGGATGTTTTGCCTAGTCATGTTGGTTACGAGA 240

50      60
M V T H L S V S L T T L L D K F S N I S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTC 300

70      80
E G L S N Y S I I D K L G K I V D D L V
TGAAGGCTTGAGTAATTATTCATCATAGACAACTTGGGAAATAGTGGATGACCTCGT 360

90      100
A C M E E N A P K N V K E S L K K P E T
GGCATGTATGGAAGAAATGCACCTAAGATGTAAAGAATCACTGAAGAAGCCAGAAC 420

110     120
R N F T P E E F S I F N R S I D A F K
TAGAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTTGATGCCTTCAA 480
```

FIG.14C-2

130 D F M V A S D T S D C V L S S T L G P E
140 GGACTTCATGGTGGCACTGACACTAGTAGTGTGTGCTCTCTTCAACATTAGGTCCTGA 540
150 K D S R V S V T K P F M L P P V A A S S
160 GAAAGATTCCAGAGTCAGTGTCAAAACCATTATGTATACCCCTGTTCAGCCAGTTC 600
170 L R N D S S S N R K A A K S P E D P G
180 CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAGCCGCAAGTCCCTGAAGACCCAGG 660
190 L Q W T A M A L P A L I S L V I G F A F
200 CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTGCGCTTGTAAATTGGCTTTGCTTT 720
210 G A L Y W K K K Q S S L T R A V E N I Q
220 TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAATATACA 780
230 I N E E D N E I S M L Q Q K E R E F Q E
240 GATTAAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGATTTCAGA 840
248 V
GGTGTAAAT 849

FIG. 15A

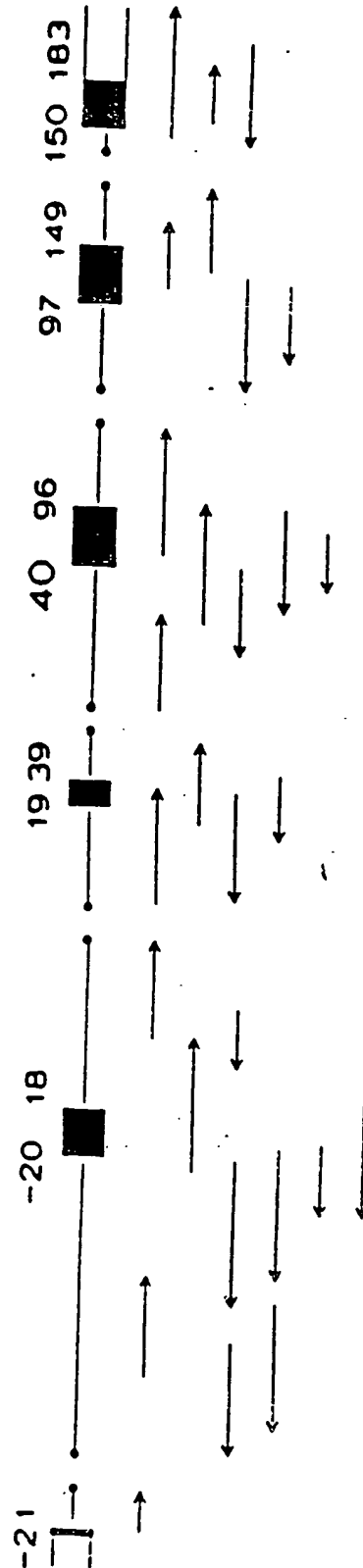


FIG.15B-1

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA 45
AAAATCGCGCCCGGTGCCCGGGGAGCCGGCGCTCCCTGGGACT 90
TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG 126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA 45
CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT 90
ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG 135
TGTTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180
TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG 225
GCTAAAAAGCTGTGTTTCAAATATTCTTTTGATGTCTCACAAAT 270
TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT 315
TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA 405
ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT 450
CTCTAGTTTTTTAGAAGATAACCCTAAGGGCTAAGTCTTTAACATGC 495
TGCTACAAGTTTATTCCCTAATTGCCATTGGGAAATTGGCTGAAGA 540
AAGTTTTTAAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT 585
CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT 630
AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT 675

FIG.15B-3

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC	45
CAAACCTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA	90
GTCTAAAAGATCTGTATTATCACTTTTTTTATTTTGAAGGATGCCT	135
TTTGATTACAGAGGGGAAATCAAGGATTAAAAATCAATATACATGT	180
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTG	225
TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA	270
	19
	ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTTTGTCTCTGTAGGTGGCAA	315
	30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM	
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA	360
	39
etAspValLeu	
TGGATGTTTTGGTATGTAACTACATTTCTGAGTTTCATTTTAGT	405
AGCTCATAGAAGAAATGGGATCATTATATTGAGATAGTACACTA	450
GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA	495
TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT	535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTAGAATAGTCCCTCCTCCT	45
CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC	90

FIG.15B-4

CTCCTATTACAACATTTTAAAGTAATGTAATATTAATTTTAAAAAT 135
CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG 180
AAGCTGAGACGGGTGGATCATTGAGGTCAGGAAGTTTGAGACAG 225
CCTGGCCAACATGGTGAACTTCCTCTCTACTAAAAATAAAAAAG 270
TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA 315
GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG 360
AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT 405
40
ProSerHisCysTrpIleS
TTTGTCTCTTTTTTTCATATCTTGCGAGCCAAGTCATTGTTGGATAA 450
50 60
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG 495
70
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA 540
80 90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA 585
96
ysGluAsnSerSerLys
AAGAAACTCATCTAAGGTAACCTTGTGTTCATTGGGATTATTTT 630
TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG 675
AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC 720
AAATTTAAAAATCTTGTTTCAGATGAGCAAAGAAAACAAGTATTTG 765
CAGTTATACTGCAATACTGAAGTGCACATTC 796

FIG.15B-5

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA	45
CTACCCTGCATTACCAATCTGAATTACATACGTTAAACAGCCAT	90
CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA	135
GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA	180
97	
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA	225
110	
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP	
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT	270
120 130	
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV	
TCTTTAGAATTTTAAATAGATCCATTGATGCCTTCAAGGACTTTG	315
140	
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS	
TAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA	360
148	
erProGluLysA	
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCAGTTCAAATGTA	405
AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG	450
TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG	495
CAGATATCAATAGCACAGAAGAAA	519

Intervening sequence of unknown length

FIG.15B-6

CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG 45

150 160
spSerArgValSerValThrLysProPheMetL
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT 90

170
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA 135

176
erAsnA
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA 180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAACTTCT 225

ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA 270

TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG 315

CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT 352

FIG.15C-1

```
-25      -20
M K K T Q T W I L T C I Y L Q
AAGCTTGCCTTTCCTTATGAAGAGACACAACTTGGATTCTCACTTGCAATTATCTTCAG 61

-10      1
L L L F N P L V K T E G I C R N R V T N
CTGCTCCTATTAACTCCTCGTCAAACTGAAGGATCTGCAGGAATCGTGTGACTAAT 121

      20      30
N V K D V T K L V A N L P K D Y M I T L
AATGTAAGACGTCACATAAATTGGTGGCAAACTCTTCCAAAAGACTACATGATAACCCCTC 181

      40      50
K Y V P G M D V L P S H C W I S E M V V
AAATATGTCCCGGATGGATGTTTGGCCAAAGTCATTGTTGGATAAGCGAGATGGTAGTA 241

      60      70
Q L S D S L T D L L D K F S N I S E G L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTTCAAATATTCTGAAGGCTTG 301

      80      90
S N Y S I I D K L V N I V D D L V E C V
AGTAATTATCCATCATAGACAACTTGTGAATATAGTGGATGACCTTGTGGAGTCCGTG 361

      100      110
K E N S S K D L K K S F K S P E P R L F
AAAGAAACTCATCTAAGGATCTAAAAAATCATTTCAAGAGCCCCAGAACCCAGGCTCTTT 421
```

FIG.15C-2

120
T P E E F F R I F N R S I D A F K D F V 130
ACTCCTGAAGAATTCTTTAGAAATTTTAAATAGATCCCATTTGATGCCCTTCAAGGACTTTGTA 481

140
V A S E T S D C V V S S T L S P E K D S 150
GTGGCATCTGAAACTAGTGTGTTGTTCTTCAACATTAAAGTCCCTGAGAAAGATTCC 541

160
R V S V T K P F M L P P V A A S S L R N 170
AGAGTCAGTGTCACAAACCATTATGTTACCCCTGTGTCAGCCAGCTCCCTTAGGAAT 601

180 183
D S S S N S K Y I Y L I
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTAAATGCATGCATGGCTCCAAT 661

TAGCACCTATAGGAGTATTGCATGGGCTTCAAGGAAACTTCTACATTATTATTATTGA 721

TACTGTTCTGTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTGTAGAAATTA 781

AATTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG 820

FIG.15D-1

GAGCTCCGAGCCCTCtCTGGCGCgCgAGGTATTTTCGTCTGTnCCCCGGGGTGCCAGGTGA	60
GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC	120
AAGCTTCGCCCTCTGCGTCCCCCGGCCCTTCGCGGTCTCCCCGCCAGTGCAGGTCCGGGGCC	180
CCCAGCGAGCGGACAAAGTTGGCCCTAATCTGCCAACACTTCTGGGGCATTTACCGTGCTC	240
TGGCCGGCCCTCCCCGATTCTTCCCTCCGGGCCCTTGCCCTGCTTCTCGCCTACCCCGGGCTC	300
CGGAAGGGAAGGAGGCGGTGTCCGGAGCAGCGGGGGGGAACCTGTATAAAGCGCCGGCGG	360
CTCAGCAGCCGGCTTCGCTCGCCGCCCTCGCGCCGAGACTAGMAGCGCTGCGGGNAGCAGG	420
GACAGTGGAGAGGCGCTCGGCTCGGGCTACCCCAATGCGTGGACTATCTGCCCGCCGCTGT	480
TGGTGCAATCTCTGGAGCTCCAGMACAGCTMAACGGAGTCGCCACACCACTGTTTGTGC	540
<div style="text-align: center;"> -25 -21 Met Lys Lys Thr Gln </div>	
TGSAATCGCTCTCTGCTTTCTGCTTATGMAAGAGACACAAAGTAGGAGGCGGCCCGGGA	600
GCTCCCAGGCTCTCCAGGAAATACTCGCGCCCGGTGCCCGGGAGCCCGCGCTCCCTGG	660
GACTTGCACTCGGGCGTGCAGGGCTGTGCTGCCGGGTGAGACAAGAGGATGCGGGGGA	720
GGCCGGCGTGGTGTGATCCCCGAGCCGAGCCGnTGAGCCAGGGAGAAAGAGTGGA	780
GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTGTAGCTGTCAG	840
TCGGAACCCGTAATCCCCGCTCTGGTGGAAAGATTGGCTTTTnGCCAGGAAATGTAAGTT	900
ATCAC	905

FIG.15D-2

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAGTTCTTGAACTCTACAGTGTAATAAGGAA	60
AAATAAGTCATGCATAAAAGCAACTATAATAÇATAATAGAAAATGTTATTTTCAAGCCGA	120
TGTGTAGGTTATGTGTGTTCCGAGAGAGAGAGAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCTTCCGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAANAAGCTGTGT	240
TTCAAAATATTCTTTTGATGTCTCACAAATTCAGTGGAAATCTCTTAGGTCTAANAATAT	300
ACATCTCTCTCACTTTAACTTGGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCMAGCAGTCTACATTTAAGTAGNATAAGATGTTTCTTT	420
TGGTGCCATTAAGGTATACATTTTATGCATTCTCTAGTTTATTAGAAATACCCCTAAGGGCT	480
AAGTCTTTAACTATGCTGCTACAAAGTTTATTCCTAATTGCCATTGGGNAATTGGCTGAAGA	540
AAGTTTTTTAACTAAAGTTAACAAATATTGTCATTGAGAGAAATAATTCNAAATGGATTTTAA	600
CTAAAGCTTTTAAAACTTTGGTGAGCATAGCTTGAATGCCGTAATATTTTAATTGCATTT	660
AAGCCAAATAACATATATAGACTGGTCTTTTGTGTCATCAAGGCATTAGATGTTAAAGT	720
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTCTGTTTTCATTTAGAC	780
-20 Th	
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG1	
TTGGATTCTCAGTTGCAATTTATCTTCAGCTGCTCCTATTATTAATCCTCTCGTCAAAACTGA	840

FIG.15D-3

1 10 18
uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu
AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAGACGTCACATAATTGGTAAGTAA 900
GGAATGCTTTACCGTGTGTAAAGAGAGCTGTGGCTCTTTTCCCTGTGCTTGTGTGAT 960
AAAAGATTTAGATTTTCTTGCCCCCAAAGTAATGTTTTCCATAAGTGGGGAAAGTAATCA 1020
CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA 1080
TTTGTGTGTAACCTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGCTCTTC 1140
TCCCCATCCTTCATAGGCAGTGAAGGACCCTTGAGAGAGTTCGCTGTGTGCTGATGGGCTTG 1200
CCCCAGCTTGTTCCTCCATATCTCTCCAGTGGGTTTCCCAGCATGTTCATATCCCCCTTCA 1260
CATGTCTTCTACTCTTCTTTTAAAGCCTAACGMAAGGMAATCTGAAATGGCTATTCTC 1320
CCAAATTCAAATTAAGCAGGMAAGACCCTGTCACATGTCAGTGGGTGTTTGCTCCTTCAGGGAA 1380
CATAGAGAGAGTGTATTCATTGCCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTACAT 1440
TGAAC'TCTTCCC'TCAGCGMAAGCATTTGCATTGCTTCCC 1479

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGGTGMAATTCAGATCATGTTCCAAACTCAGTAGGT 60
TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAGATCTGTATTATCACTTTTTTA 120
TTTTGAAGGATGCCCTTTTGATTACAGAGGGGAAATCAAGGATTAAAAATCAATATACATGT 180

FIG.15D-4

```

AAATATTGAAATTCATTGGTAACCTTTAAANAAGCACACAGTTTTGTGTGCTTTTCTCTCCAA      240
AGCACTACAAATATATGATTAAATTGATGTATAGAATTTTCTTATGGAAATTTTTTTTTTTGT      300
                                     30
ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
CTCTGTAGGTGGCAAAATCTTCCAAAAGACTACATGATNACCCCTCAAAATATGTCCCCCGGA      360
                                     39
etAspValLeu
TGGATGTTTTTGGTATGTAAACTACATTTCTGAGTTTTCATTTTAGTAGCTCATAGAGAAA      420
TGGGATCATATTTGAGATAGTACACTAGCTGTCTATTTAGGAGCTTGCTTATTGTCTAG      480
GATTTGAAAGNAATTTATCTTTTGGMAATTTTGACTTGCAGGCTTTTTTTTCCCCCTCTT      535
                                     Intervening sequence of unknown length
CCTGTTACAAATATTCCTCCTCCTATTACANTAGTCCCTCCTCCTGTCACTAGTC      60
CCTTCTCTTTCTTCTTACAAATAACCCCTGTCTCCTATTACAAACATTTTAAGTAATGTAAT      120
ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTTCATGCTTGTAATCCCAGCACATTTGGG      180
AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAAACATGGT      240
GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACCTTGTAAT      300
CTGAGCTACTCGAGAGGCTGAGGCAGGAGAAATCACTTGAGTAACATAAACGATAGCTTTG      360
AAGAGTACTCCGAGTTTTTATGGCACTTACTTATTAATAATAGCTGTTTTGTCTCTTTTTC      420
```


FIG.15D-5

40	ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL	50	
	ATATCTTGCAGCCCAAGTCATTGTTGGATNAGCGAGATGGTAGTACAAATTGTCAGACAGCT		480
60			
	euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	70	
	TGACTGATCTTCTGGACAAAGTTTTTCAMATATTTCTGAAGGCTTGAGTAATTATTCCCATCA		540
80			
	leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL	90	
	TAGACMAACTTGTGAATATAGTGGATGACCTTGTGGAGTGGTGMAAGMAAATCATCTA		600
96			
ys			
	AGGTAACTTTGTGTTCAATTGGGATTATTTTTTCATTACGCTTCTCTMAAACCCTATGCTTC		660
	TTGGTGCTGTTGGGGAAATGAGGCACCTTTATTTATGATATTTTGATTTGTATAAACTTC		720
	AAATTTAAAAATCTTGTTCAGATGAGCMAAGMAACMAAGTATTTCAGTTATATACTGCAAT		780
	ACTGMAAGTGCAATTC		796
	Intervening sequence of unknown length		
	TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCCTGGGATCACTACCCCTGCATTACC		60
	AATCTGAATTACATACGTTAAACAGCCATCTAAAGTGCTAGTTGTAGAGTCTAATA		120
	CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCCTCAGTTAAGTCTGAAGA		180
	97		
	AspLeuLysLysSerPheLysSerP		
	CTATTTGAAAAATGTAATCCTATTTTTTCTCTAGGATCTAAAAAATCATTTCAAGAGCC		240

FIG.15D-6

```

110      roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
120      CAGAACCCAGGCTCTTTACTCCTGAGAAATTTCTTAGAAATTTTAAATAGATCCATTTGATG
300
130      laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
140      CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA
360
148      erProGluLysA
      GTCCCTGAGAAAGGTAAGACATGTAAAGCATTTCCAGTTCAAAATGTAAACAACTTAA
420
      TCTTCCCTATGTAGTAAGAAATCTACCTCTGTGTGTTAAGCTGTAGCAAGATACATGCAATGTA
480
      CGCTAATAAAGCAGATATCAATAGCACAGMAGAACTAATGATTGTAGATTTGTGGG
541
      Intervening sequence of unknown length

      CTCTATATACCAATCACCATATACACTGACACATTATTGCTTTCTATTAGATT
60      spS
150      erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
      CCAGAGTCAGTGTACAAAACCATTTATGTTACCCCTGTTGCAGCCAGCTCCCTTAGGA
120
170      snAspSerSerSerSerAsna
      ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA
180
      ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATT
240
      GATACTGTTCTGTACTGTATTCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAAT
300
```

TAAATTTCCCTAGAGCTGGAGATAATGTTTAGAGAAATTAGGCCAATAAATTTTCTGCTGA	360
GGTTATTTTAAATAGACATAMAAATTAATTTTAGAATAATGATTTATGCCCTTTTGTTGMA	420
TCATTAACATATAT	434
Intervening sequence of unknown length	
ACAGAAACAGTTAAACAACACAGCATMAGAGNAAACTTCTAGAAATGGATATGCTGTA	60
178	
rgLysAlaLysAsnProGlyAspSerSerL	
TTCATCAGTGTGTTCTTTAAATTTATAGGMAAGGCCAAMAAATCCCCCTGGAGACTCCAGCC	120
190	
eullisTrpAlaAlaMetAlaLeuProAlaIleuPheSerLeuIleIleGlyPheAlaPheG	200
TACACTGGCCAGACATGGCAATTGCCAGCATTTGTTTCTCTTATAAATTGGCTTTGCTTTTG	180
213	
lyAlaLeuTyrTrpLys	
GAGCCTTATACGGAAAGGTAAAGTGGTACCATTCCCTTTTMAAATATGCTATGTCTAC	240
ATAAATTATCATCTTTTTTCCCTCAAGAAATGATCCCTTtAAGAAACAGTGAATCTACCT	300
TAGCTTATACTAAACAATAATTTAATTTTATAAAGTTTCCCTGTTTCTCATTTATGTCTGGA	360
GACAATCCCCTCTAGCTGATAATTCACGCTTAAGAAATTAGGAACT	404
Intervening sequence of unknown length	

FIG.15D-8

```

AAACTGTTATTGGAGTTATTGCCATAAAGATAAAMAGTGGAGTCCACTTACCTCTTAA 60
      214
TATTAGACCATTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTCCAGAAGAGAC 120
      LysArgG
      230
InProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS 235
AGCCAAGTCTTACAAGGGCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA 180
e
GGTATTTTGTGTTTGGCTAAATGTGTGCCCAATCAAGCATGACATTGCCATTTTCACACACTG 240
TGTACCTGCCCATTAATGTCTTTAAAGMAGTCCTTCACCTCATGACAGTAGCTCCTAACCAGT 300
GAGTCCCCAACTCTATCCATGTTTCTGTATGTCTCACTCTCTCTTC 344

      Intervening sequence of unknown length

GTATGTGTATATATCATATACAGAGAAAGAAATGTTTAACTACTTGGMAAGACTACCTTA 60
AGACAAATGAAAGTCTTCCCTCTATAGTAATAAGAGGTAGGCTCCCCCATTCMAT 120
TTTGCAATCTTCTGCTACTATATTTACAGAAAGCTGCCTTTACAAATGCCGAGATCATG 180
GTGTACCTCAGAAATCTCTGACCAAGAGCAATAAGCATTTTCTTATTTGTTTTCAGTA 240
      rM
237      248
etLeuGlnGluLysGluArgGluPheGlnGluVal
TGTTCAGAGAGAAAGAGAGAGAGTTTCAAGAAGTGTAAATGTGGCTTGATCAACACTGT 300
TACTTTCGTACATTGGTAAGTTTTTTTCTCTTTTCCCTTTTCTTTCTTTTATTTATATA 360
```

FIG.15D-9

CTTTAAGTTCTAGGGTACATGTGCGCACAAATGTGCGAGGTTTGTGTACGTATGTTTACATGTGC 420
CATGTT 426

FIG.16A

-25
Human MKKTQTWILT C1YLQLLLEN PLVKTEGICR NRVTNNVKDV TKLVANLPKD 25
Monkey MKKTQTWILT C1YLQLLLEN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Dog MKKTQTWIIIT C1YLQLLLEN PLVKTGIGC KRVTDVVDV TKLVANLPKD
Cat MKXTQTWIVT C1YLQXLLLEN PLVKTGICR NRVTDVVDV TKLVANLPKD
Cow MKKTQTWIIIT C1YLQLLLEN PLVHTQGICS NRVTDVVDV TKLVANLPKD
Rat MKKTQTWIIIT C1YLQLLLEN PLVKTQEICR NPVTDNVKDI TKLVANLPND
Mouse MKKTQTWIIIT C1YLQLLLEN PLVKTREICG NPVTDNVKDI TKLVANLPND
Chicken TWIIIT CFCLQLLLEN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND
Scfpep MKKTQTWIIIT C1YLQLLLEN PLVkt.gicr nrvtd.vkdv tklvanlpkd

26
Human YMITLKYVPG MDVLP SHCWI SEMVQLSDS LTDLDDKFSN ISEG...LSN 72
Monkey YMITLKYVPG MDVLP SHCWI SEMVQLSDS LTDLDDKFSN ISEG...LSN
Dog YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDLDDKFSN ISEG...LSN
Cat YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDLDDKFSN ISEG...LSN
Cow YMITLKYVPG MDVLP SHCWI SEMVEQLSVS LTDLDDKFSN ISEG...LSN
Rat YMITLNYVAG MDVLP SHCWL RDMVTHLSVS LTTLDDKFSN ISEG...LSN
Mouse YMITLNYVAG MDVLP SHCWL RDMVIQLSLS LTTLDDKFSN ISEG...LSN
Chicken YLITLKYVPG MDVLP SHCWL HLMVPEFSRS LHNLLQKFSN ISEG...LSN
Scfpep YmitLkYVpg MDvLP SHCWI semveqlsvs LtddlDKFSn Iseg...LSN

73
Human YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLET PEEFFRIFNR 121
Monkey YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLET PEEFFRIFNR
Dog YSIIDKLVKI VDDLVECTEG YSFEN.VKKA PKSPELRLET PEEFFRIFNR
Cat YSIIDKLVKI VDDLVECVKE HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Cow YCIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Rat YSIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Mouse YSIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Chicken YSIINNLTTRI INDLMACLAF DNKDFEIKEN GHLYEEDRFI PENFFRIFN3
Scfpep YsiIdkLvki vddlveC.ee nsakn.vRks .kspEprlEt PEEFFRIFNR

FIG. 16B

122 Human SIDAfKDF.V VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR 169
 Monkey SIDAfKDF.A VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
 Dog SIDAfKDF.L VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
 Cat SIDAfKDF.L VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
 Cow SIDAfKDF.L VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
 Rat SIDAfKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
 Mouse SIDAfKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
 Chicken TIEVYREFAD SLDK.NDCIM PSTVETPEND SRVAVTKTIS FPPVAASSLR
 Scfpep sIdafKdf.m vAsktadCvv sStl.sPeKd SRVSVTKpfm LPPVAASSLR

170 Human NDSSSSNRKA KNPPGD.... ..SSLIWAAM ALPAFFSLII GFaFGALYWK 213
 Monkey NDSSSSNRKA KNPTGD.... ..SSLIWAAM ALPAFFSLII GFaFGALYWK
 Dog NDSSSSNRKA SNSIGD.... ..SNLQWAAM ALPAFFSLVI GFaFGALYWK
 Cat NDSSSSNRKX TNPIED.... ..SSIQWAVM ALPAFFSLVI GFaFGALYWK
 Cow NDSSSSNRKA SNSIED.... ..SSLQWAAV ALPAFFSLVI GFaFGALYWK
 Rat NDSSSSNRKA AKSPED.... ..PGLQWTAM ALPALISLVI GFaFGALYWK
 Mouse NDSSSSNRKA AKAPED.... ..SGLQWTAM ALPALISLVI GFaFGALYWK
 Chicken NDIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLII GFILGAIYWK
 Scfpep NDsSsSNrka .n..ed.... ..sSlqwaam ALpalfSLVI GFaFGALYWK

214 Human KRQPSLTRAV ENIQIN...E EDNEISMLQE KEREfQEV 248
 Monkey KRQPSLTRAV ENIQIN...E EDNEISMLQE KEREfQEV
 Dog KRQPNLTRTV ENIQIN...E EDNEISMLQE KEREfQEV
 Cat KRQPNLTRTV ENIQIN...E EDNEISMLQE KEREfQEV
 Cow KRQPNLTRTV ENRQIN...E EDNEISMLQE KEREfQEV
 Rat KRQSSLTRAV ENIQIN...E EDNEISMLQK KEREfQEV
 Mouse KRQSSLTRAV ENIQIN...E EDNEISMLQK KEREfQEV
 Chicken KTHPKSRPES NETIQCHGCQ EENEISMLQK KEREHLQV
 Scfpep KkqpSLtrav eniqin...e edNEISMLQe KEREfQEV

FIG. 16C

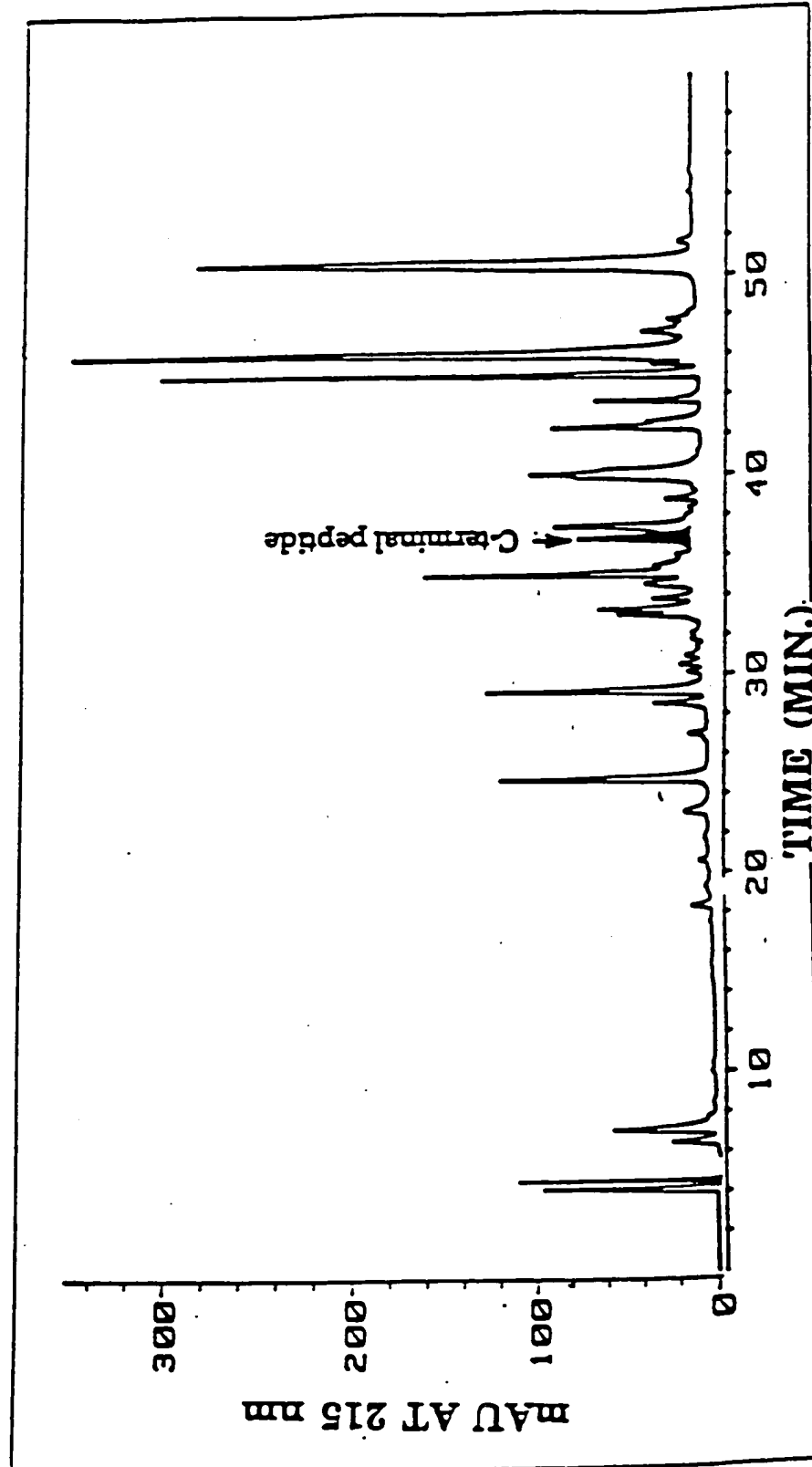


FIG. 16D

EcoRI

ta a t t taa t t c g t a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
 E F F R I F N R S I D A F K D F V

g a t tagt t t g t a at a ag t g
 GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
 V A S E T S D C V V S S T L S P E

BstEII

t a a cagt c a a t t a c t . a
 AAAGACTCCCGTGTTTCCGTTACCAAACCGTTTCATGCTGCCGCCGGTTGCT
 K D S R V S V T K P F M L P P V A

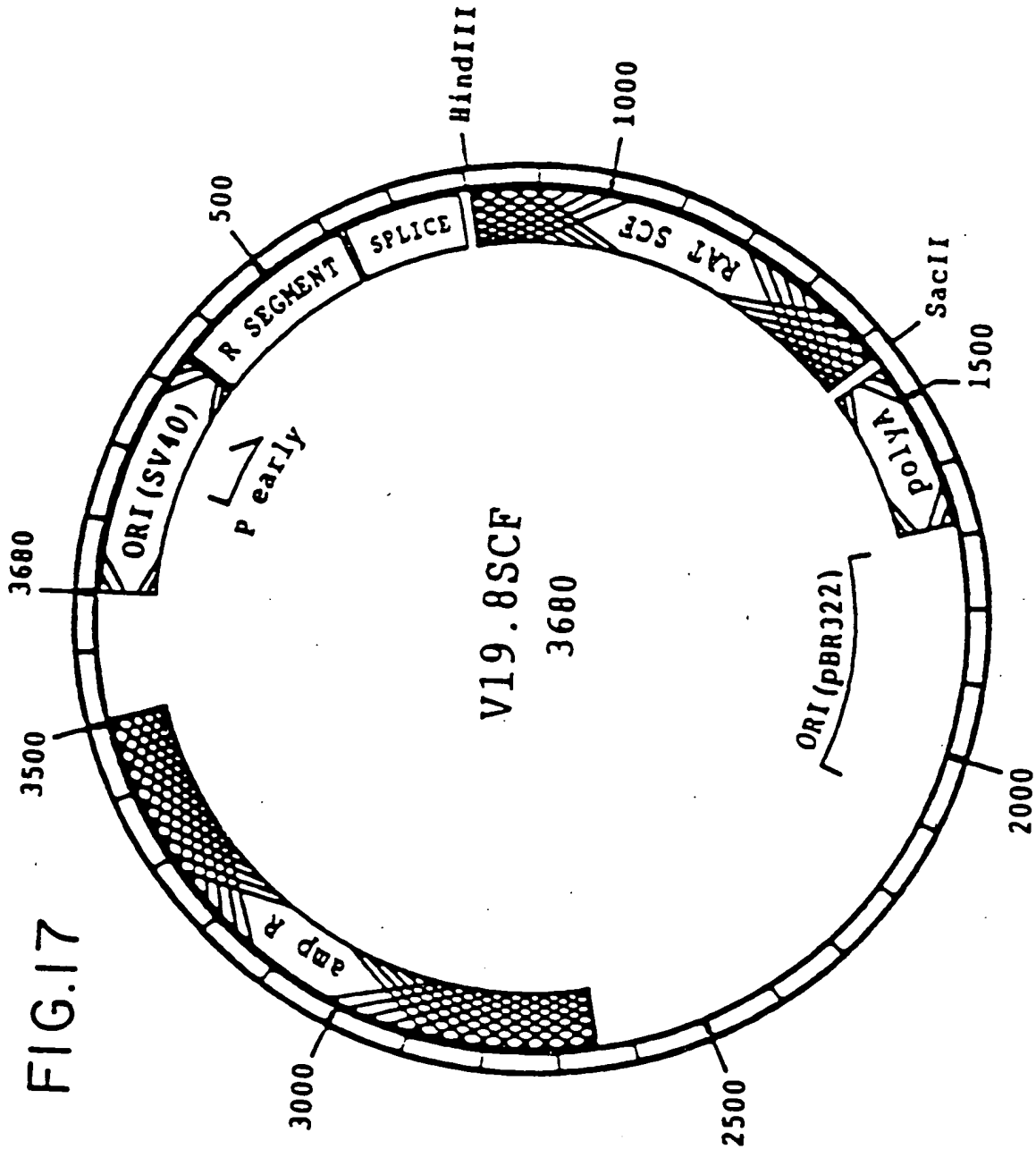
cag tag t ag agtag agt tagt g a t
 GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACCTCCAAATACATCTAC
 A S S L R N D S S S S N S K Y I Y

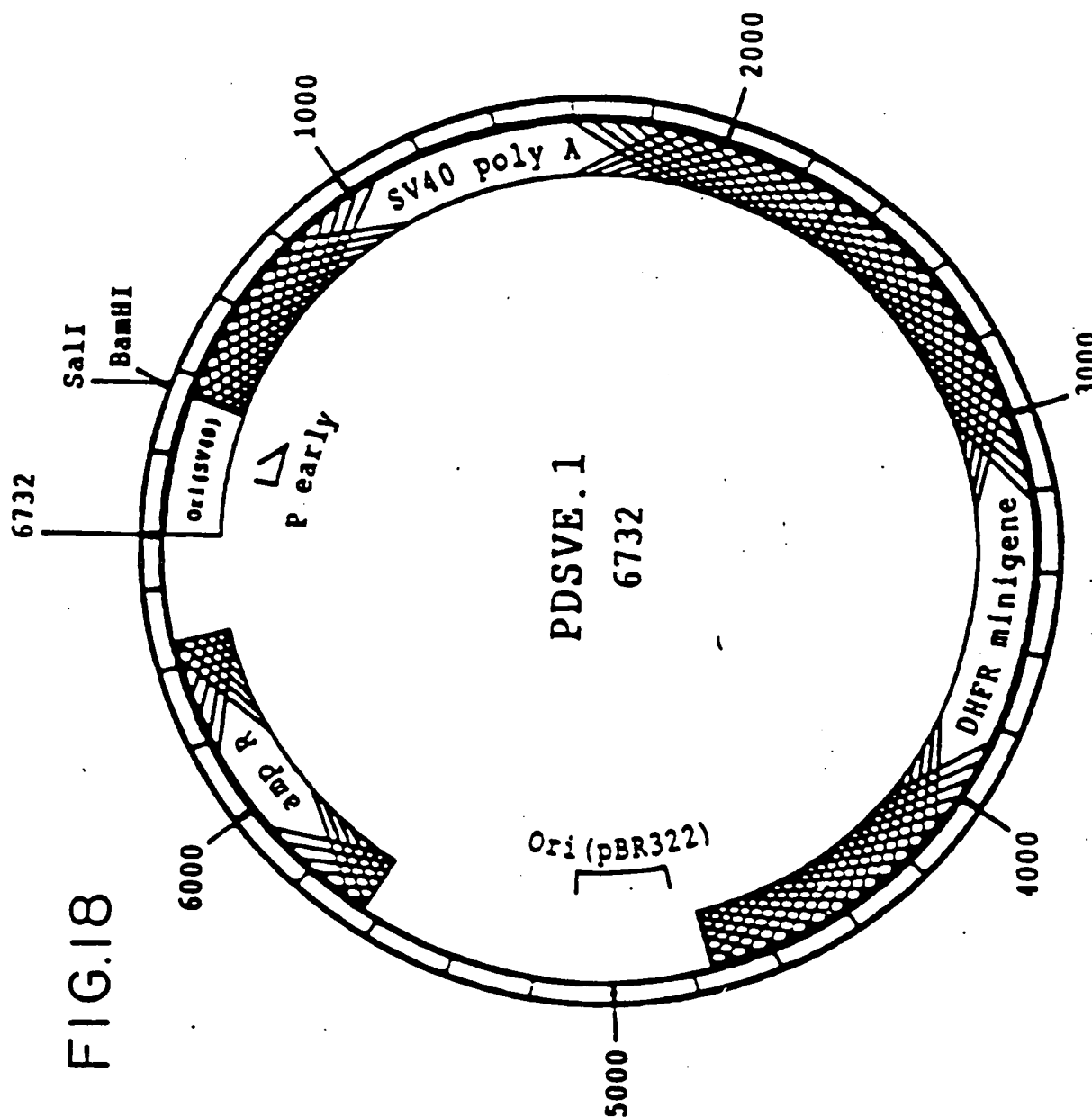
BamHI

t
 CTGATCTAATAGGATCC
 L I . .

FIG. 16E

BstEII
GGTTACCAAACCGTTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC BamHI
V T K P F M L P P V A A . .





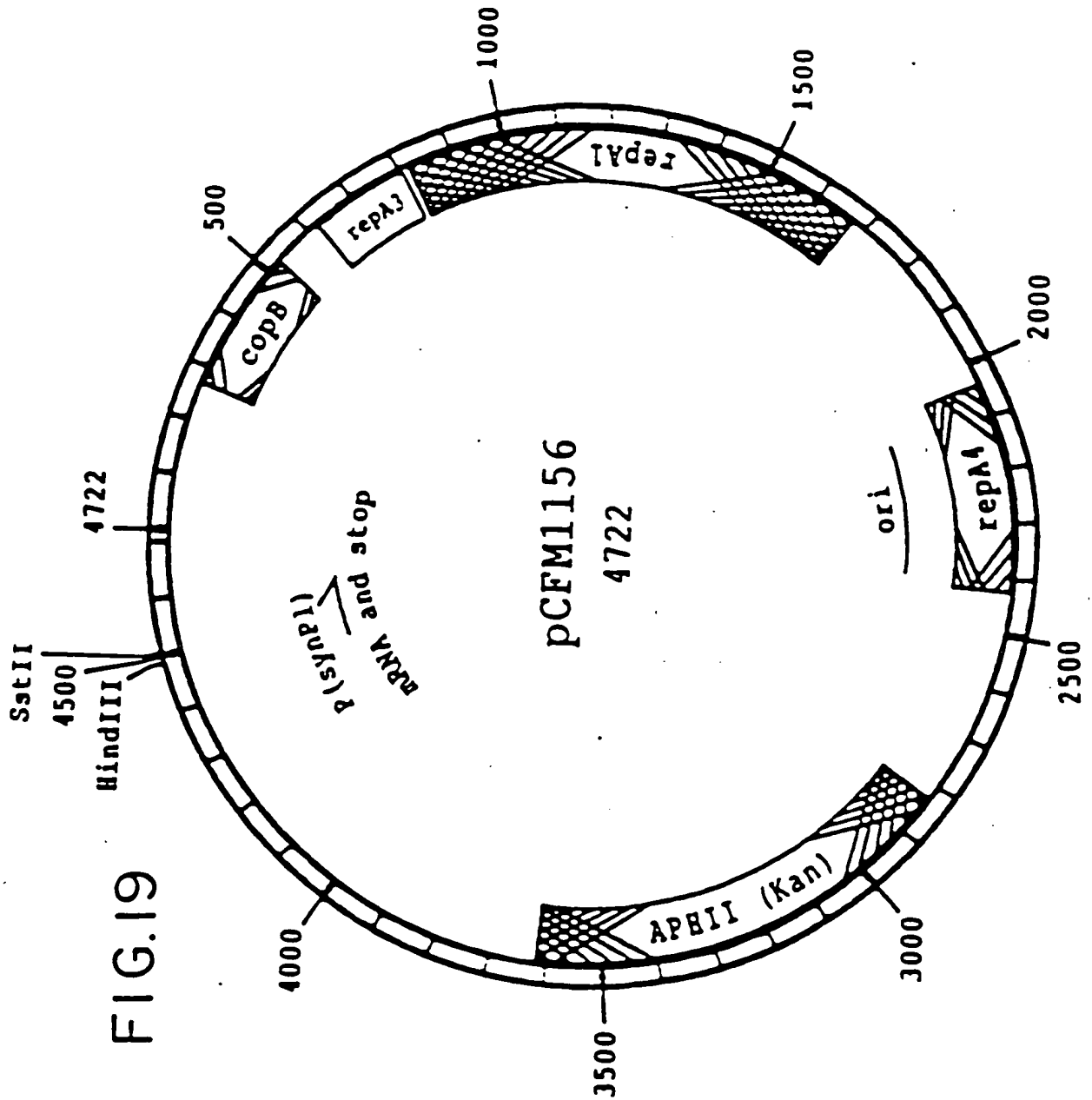


FIG. 20A

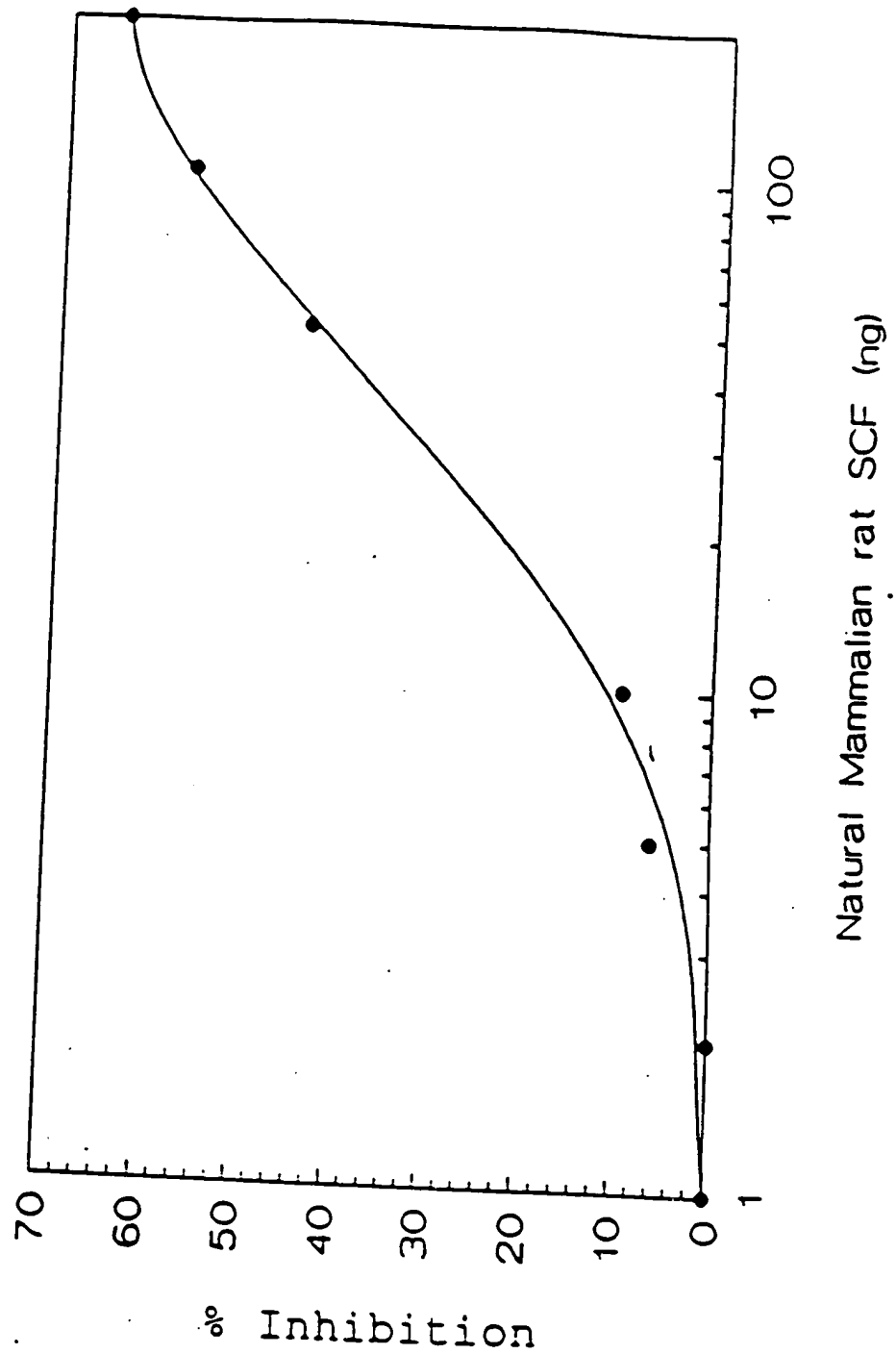


FIG. 20B

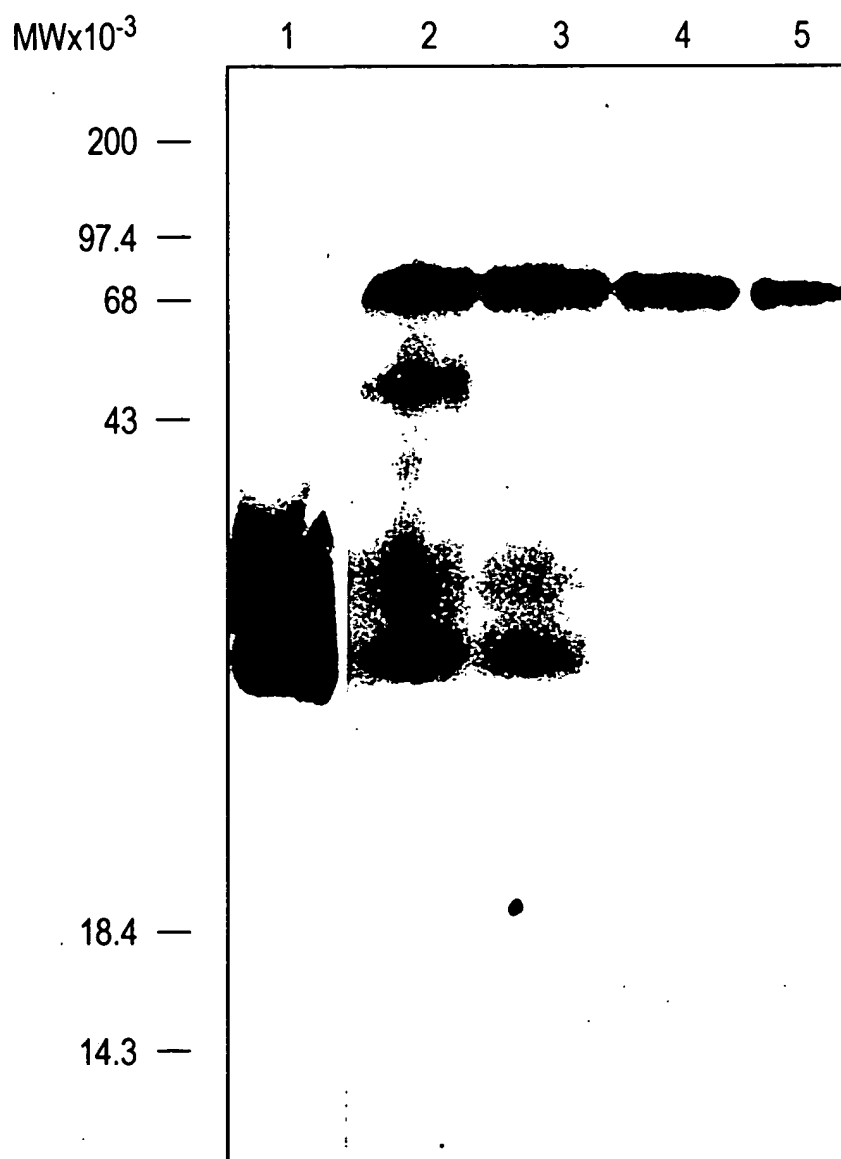


FIG. 21

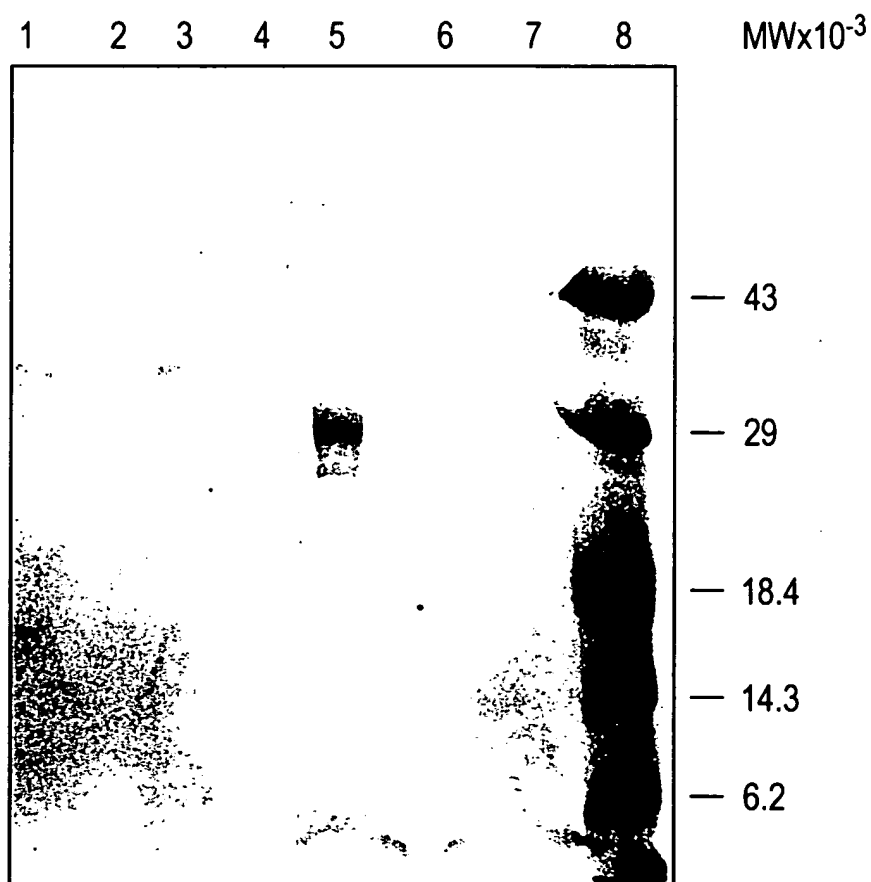


FIG. 22

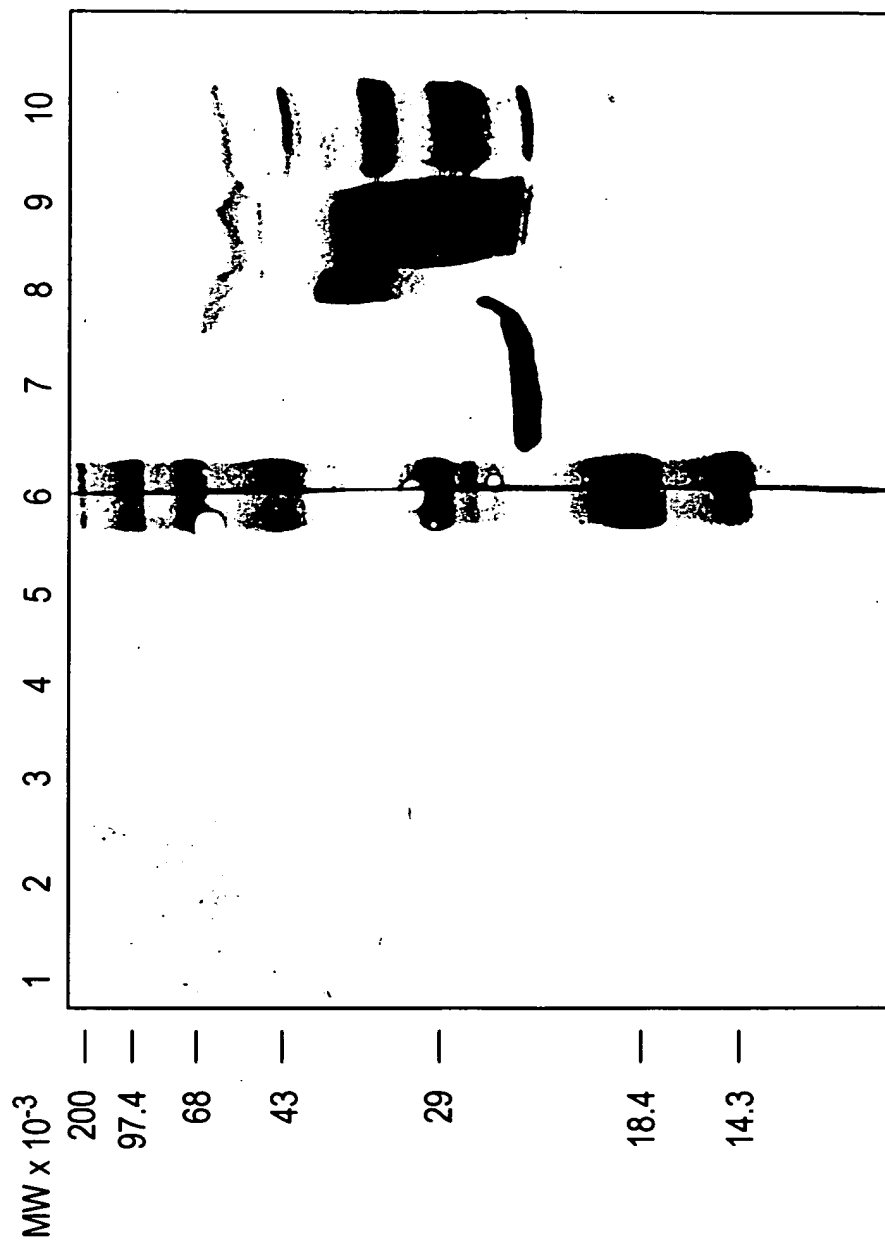


FIG. 22A

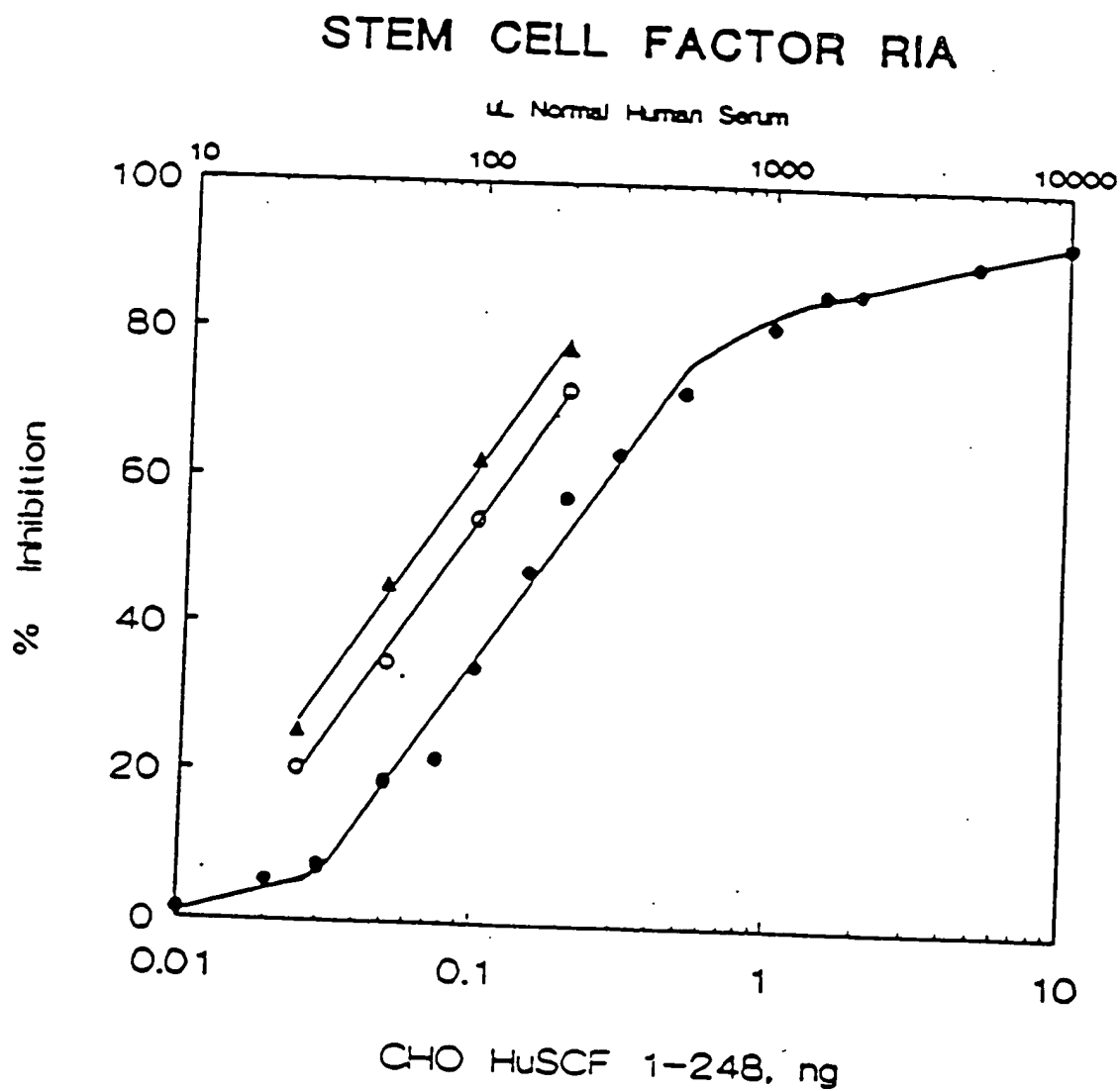
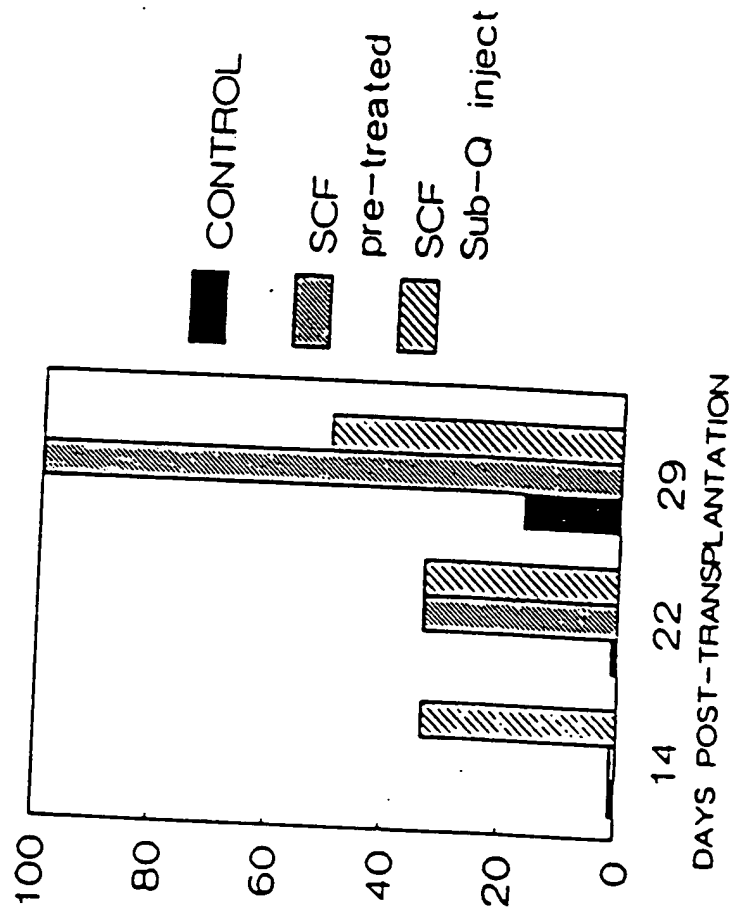


FIG. 23



% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

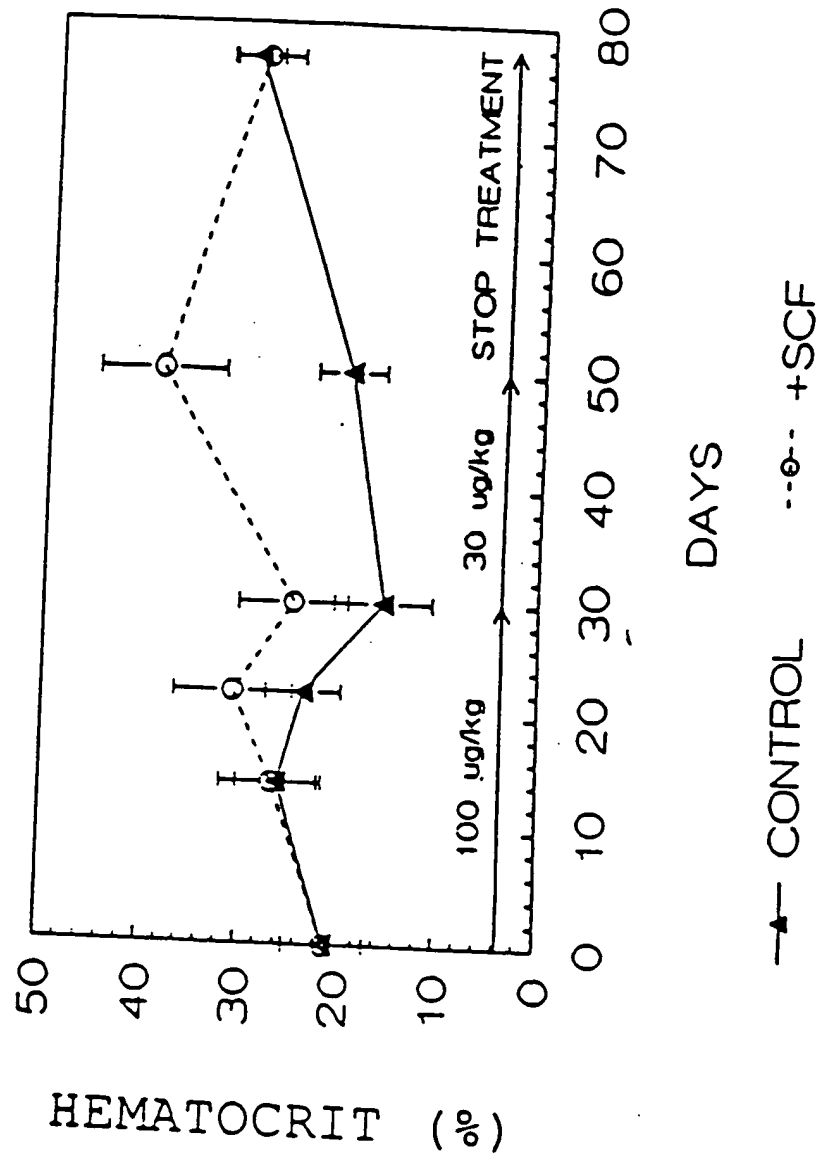


FIG. 24B

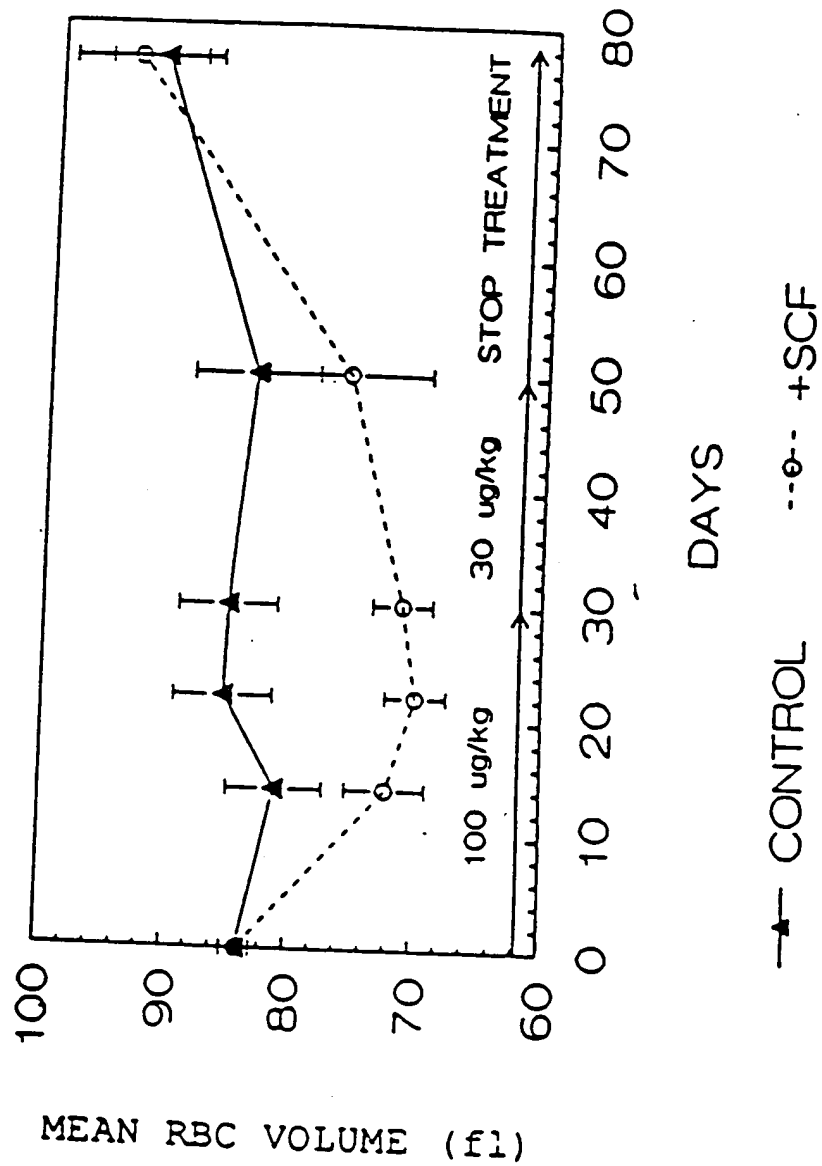


FIG. 25

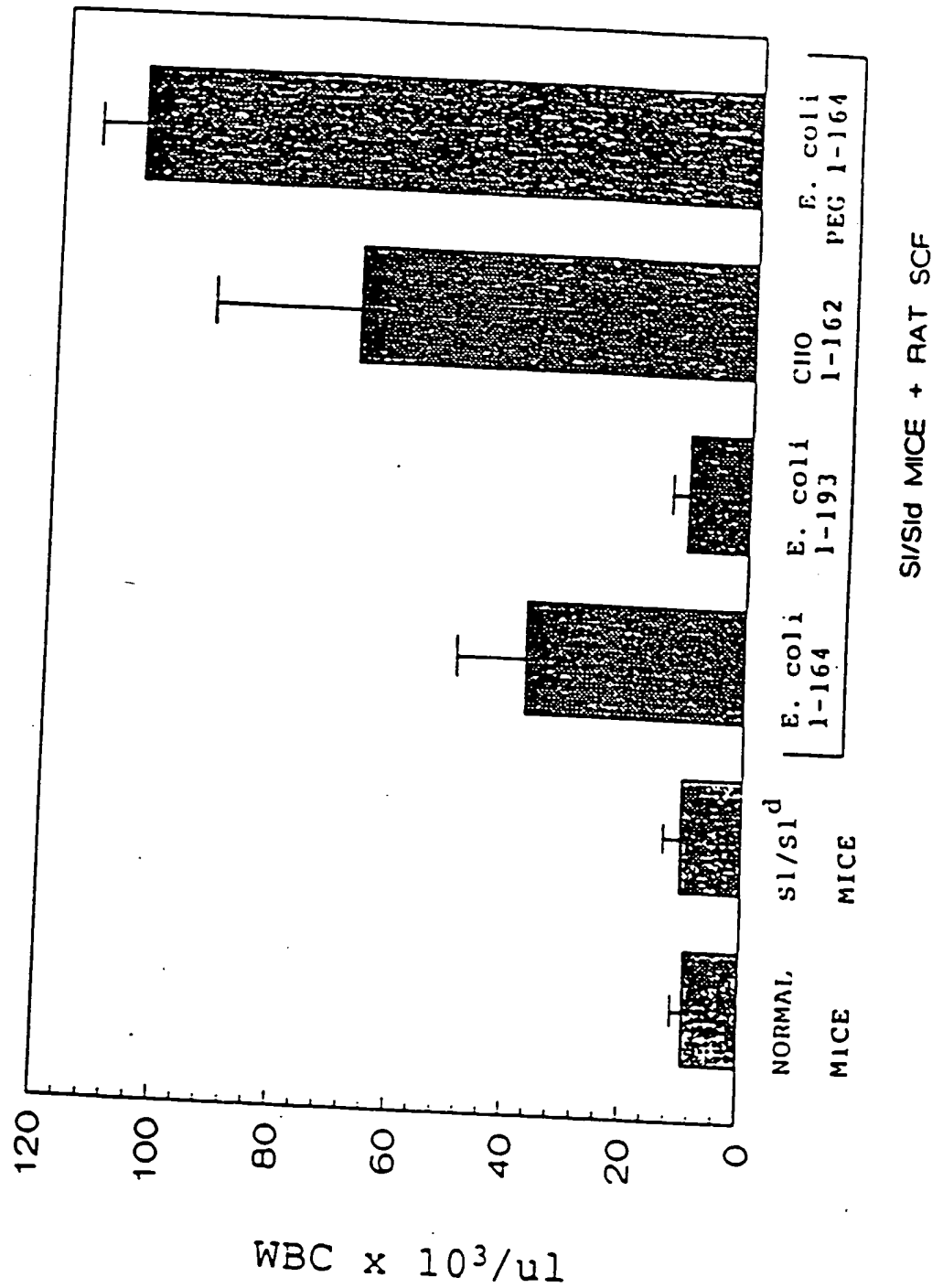


FIG. 26

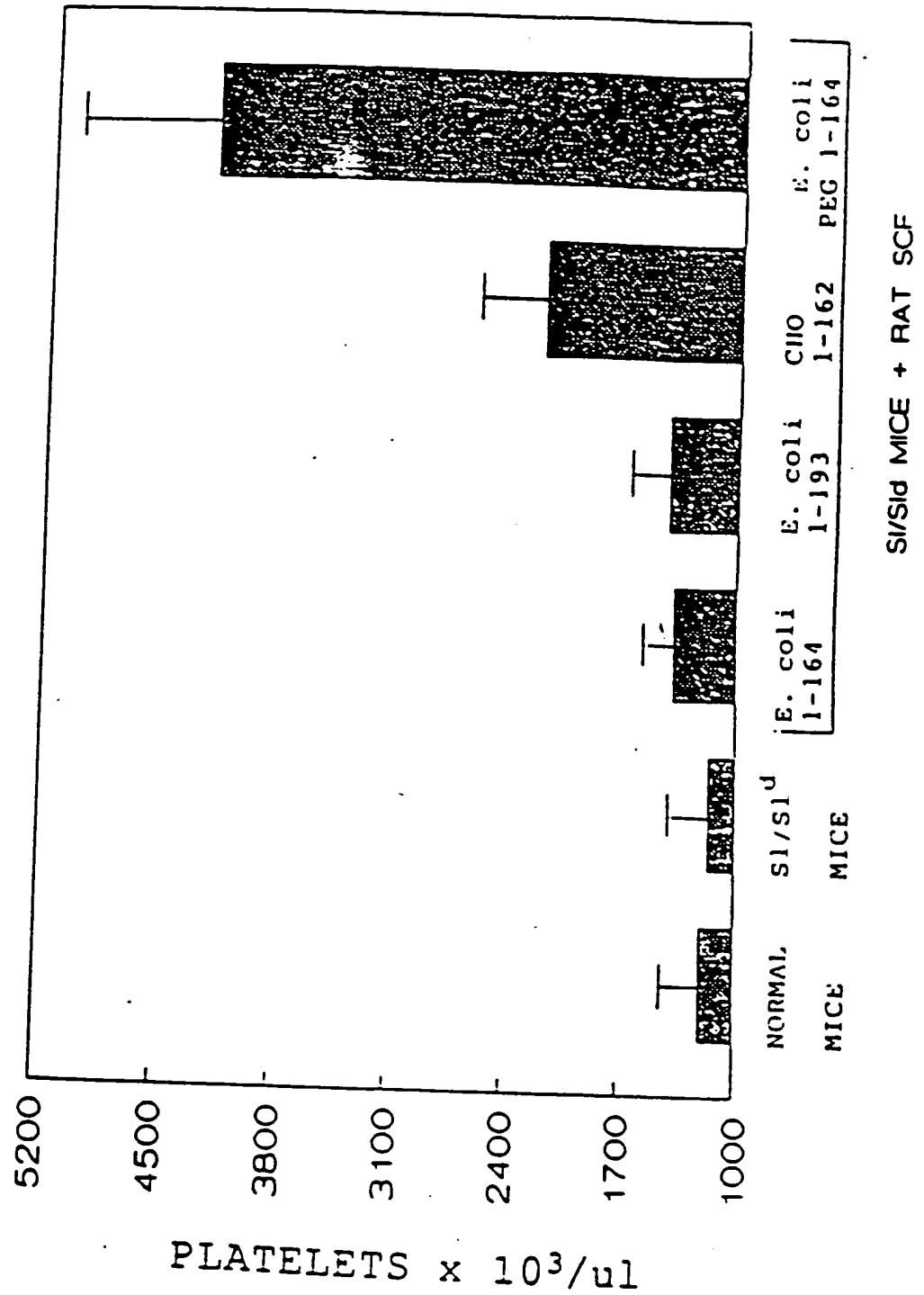


FIG. 27

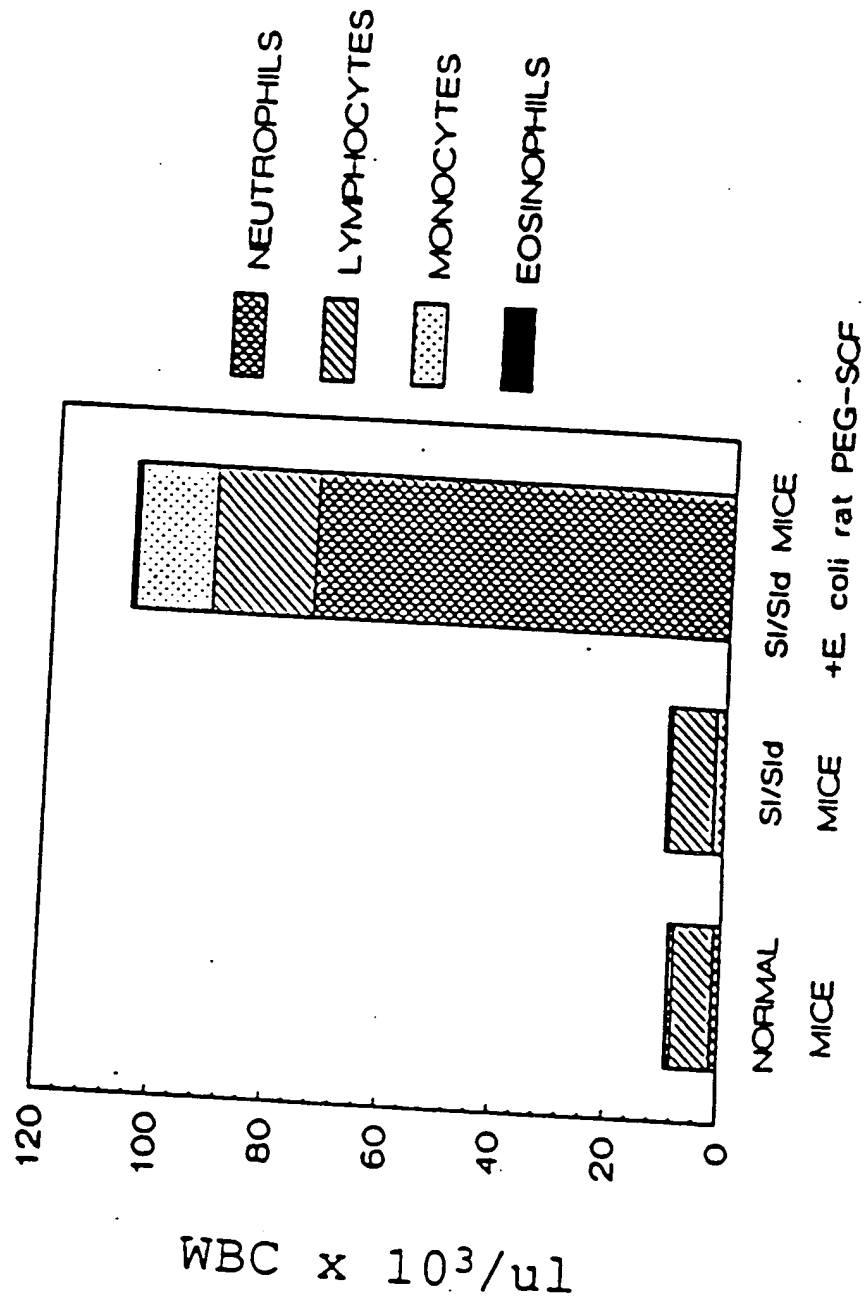


FIG. 28

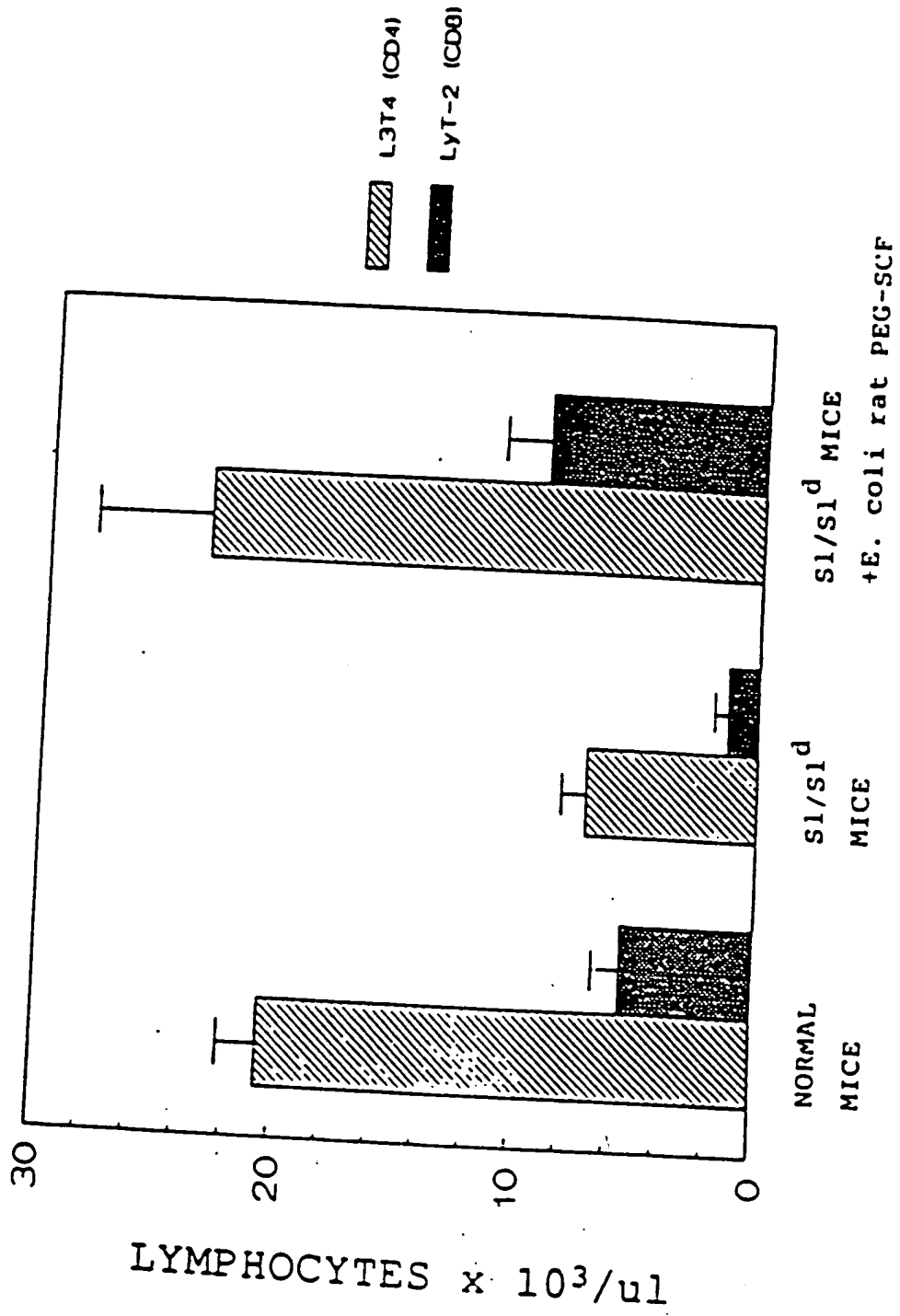
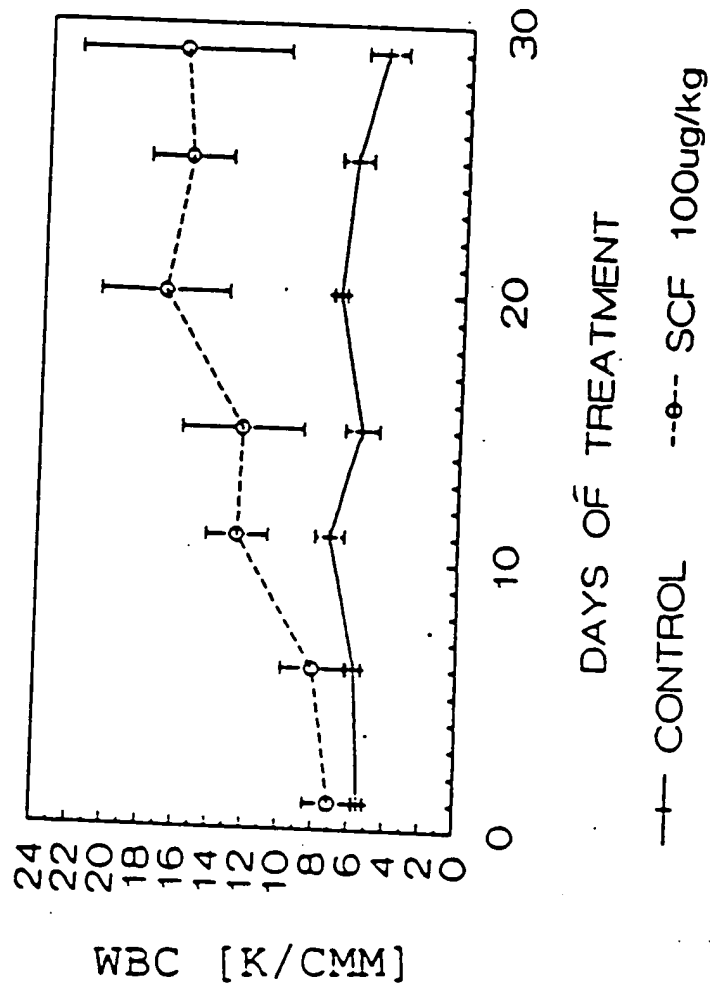
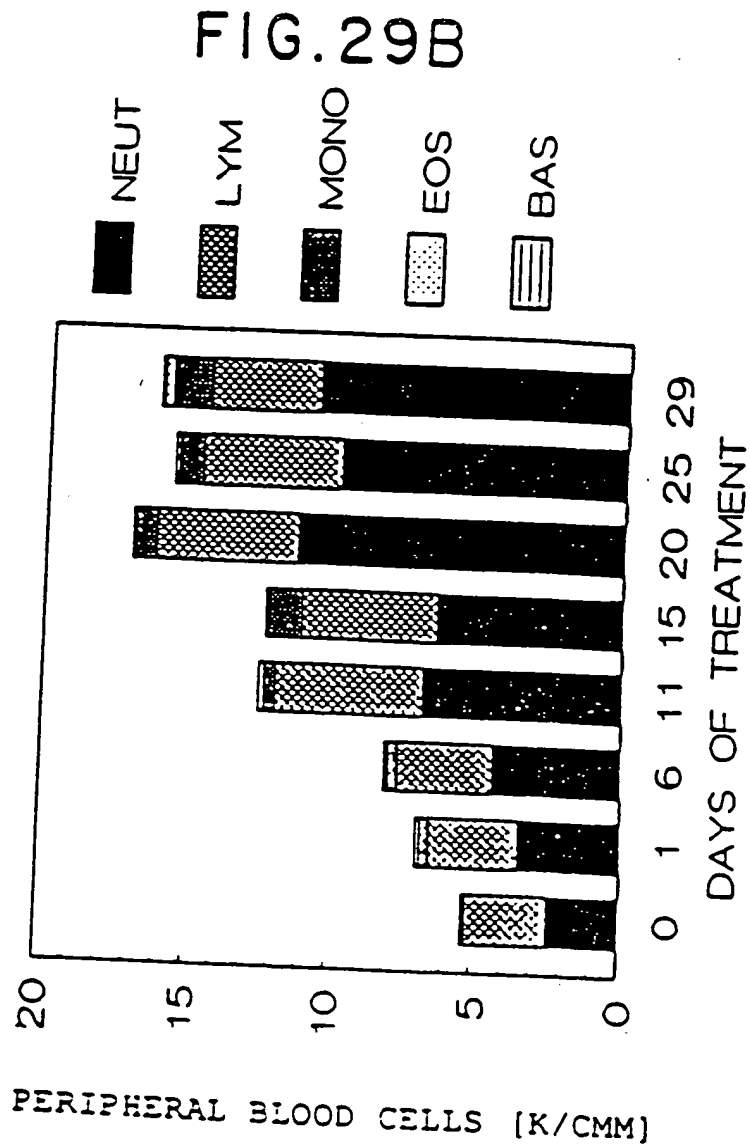


FIG. 29A





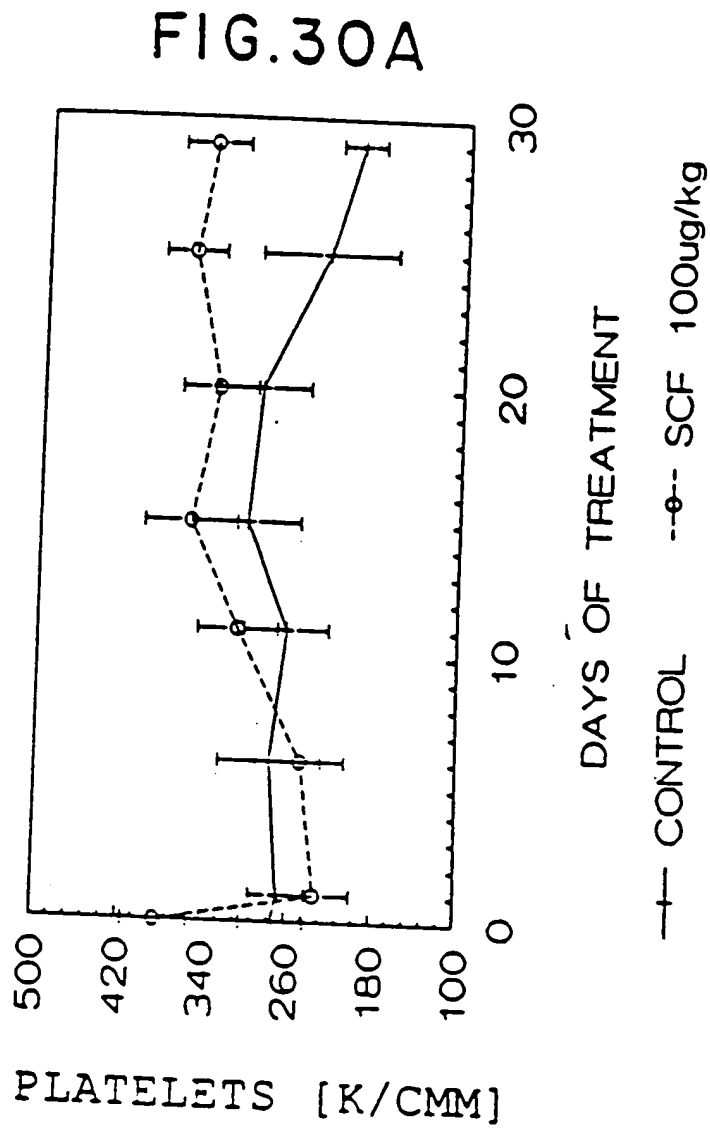


FIG. 30B

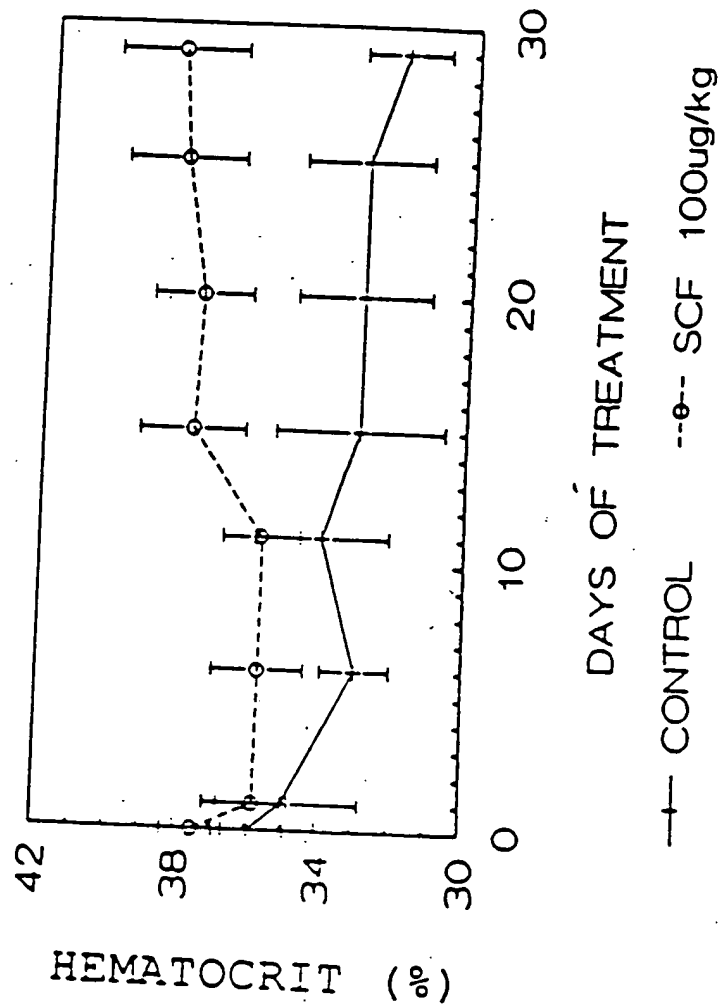


FIG. 31B



FIG. 31A

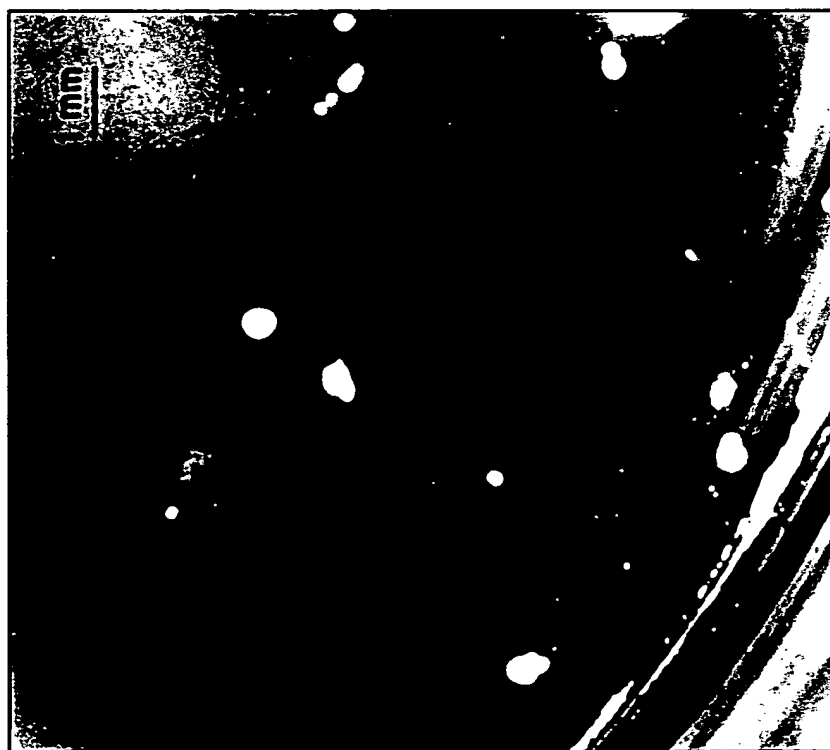


FIG. 31C

SCF4 SMP4

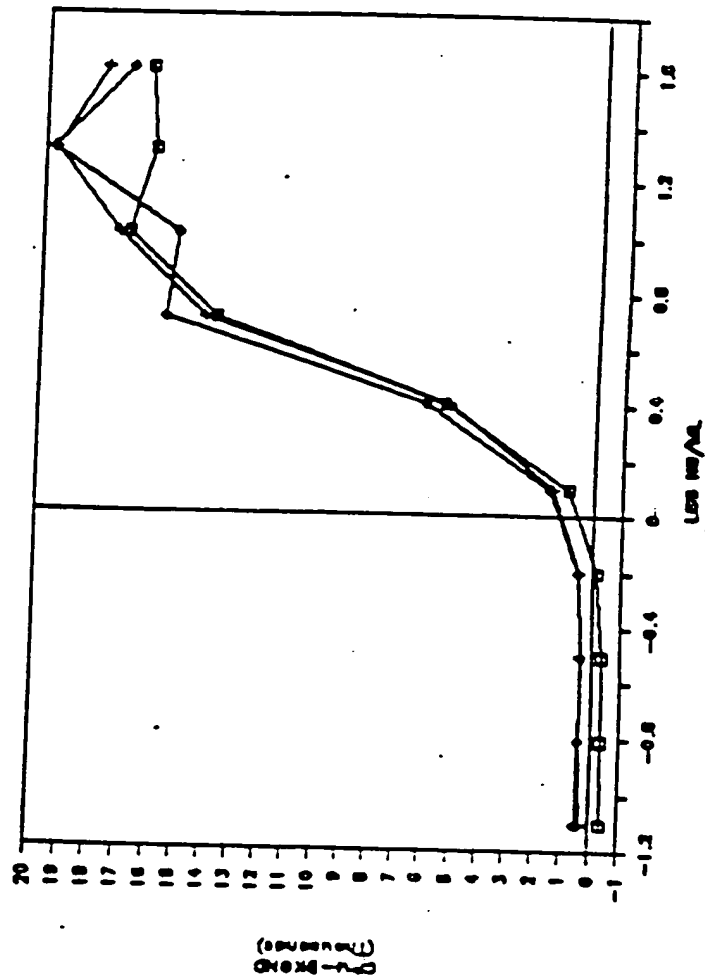
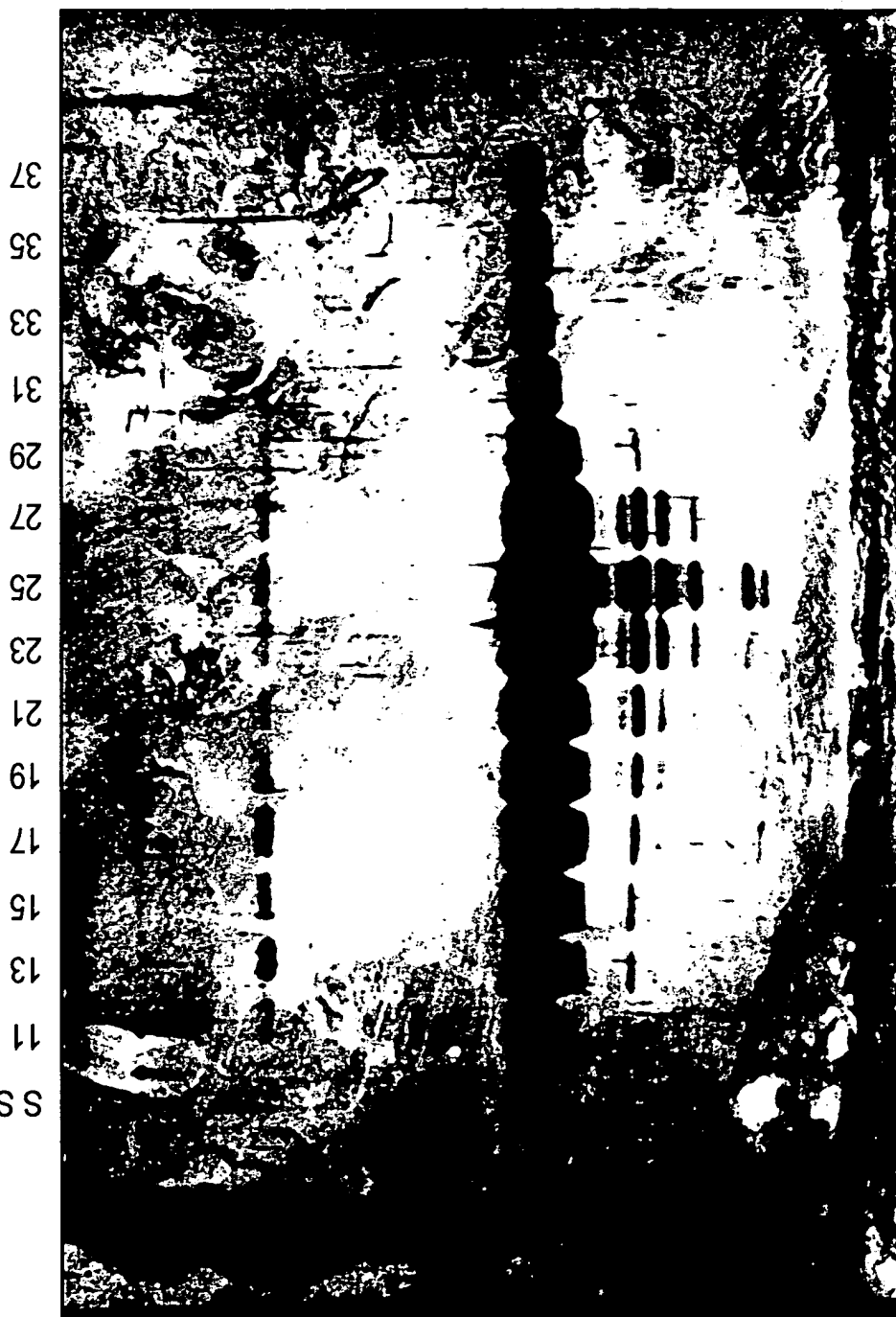


FIG. 32A

S Sepharose Load



97.4 —
 66.2 —
 42.7 —
 31.1 —
 21.5 —
 14.4 —

FIG. 32B

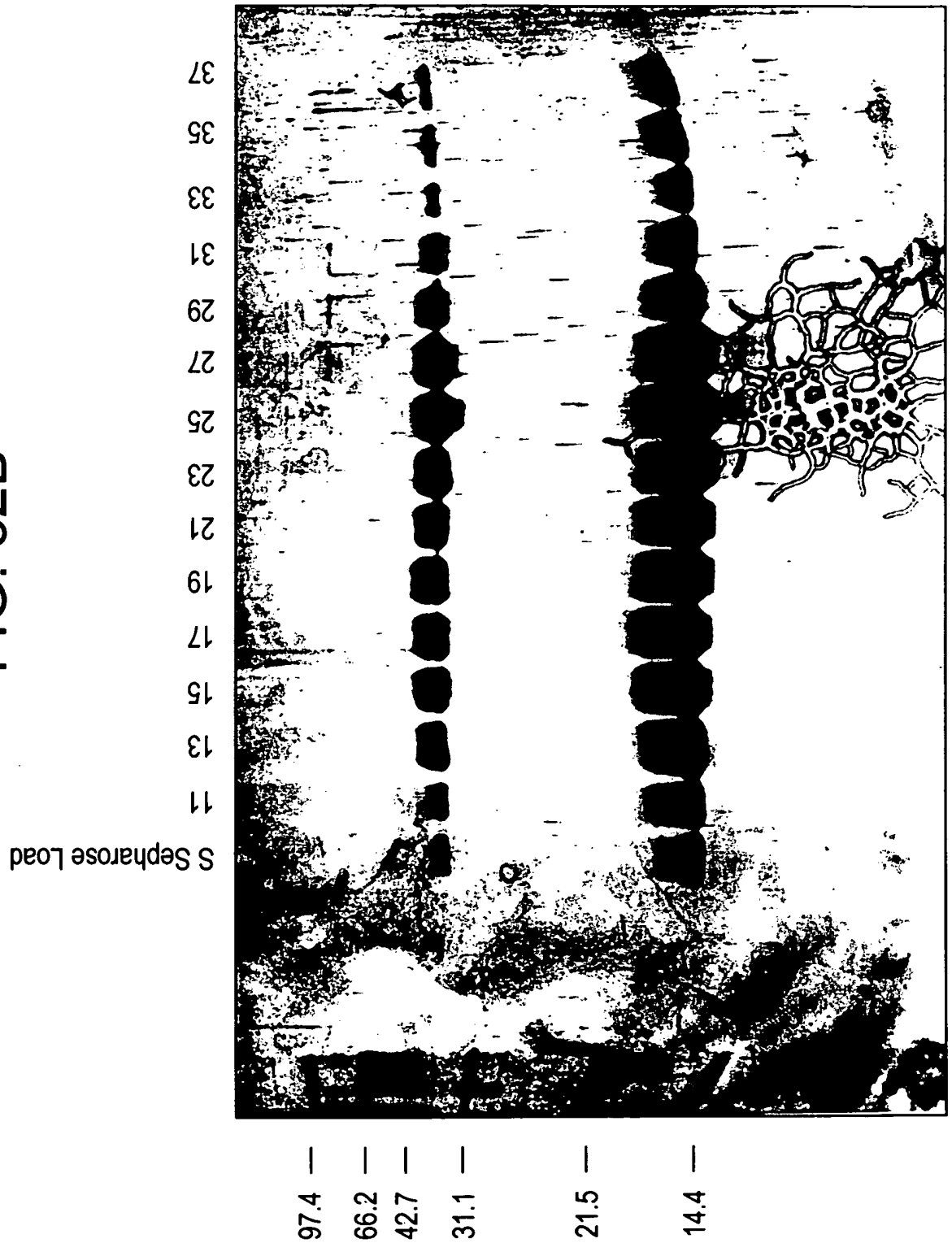


FIG. 33

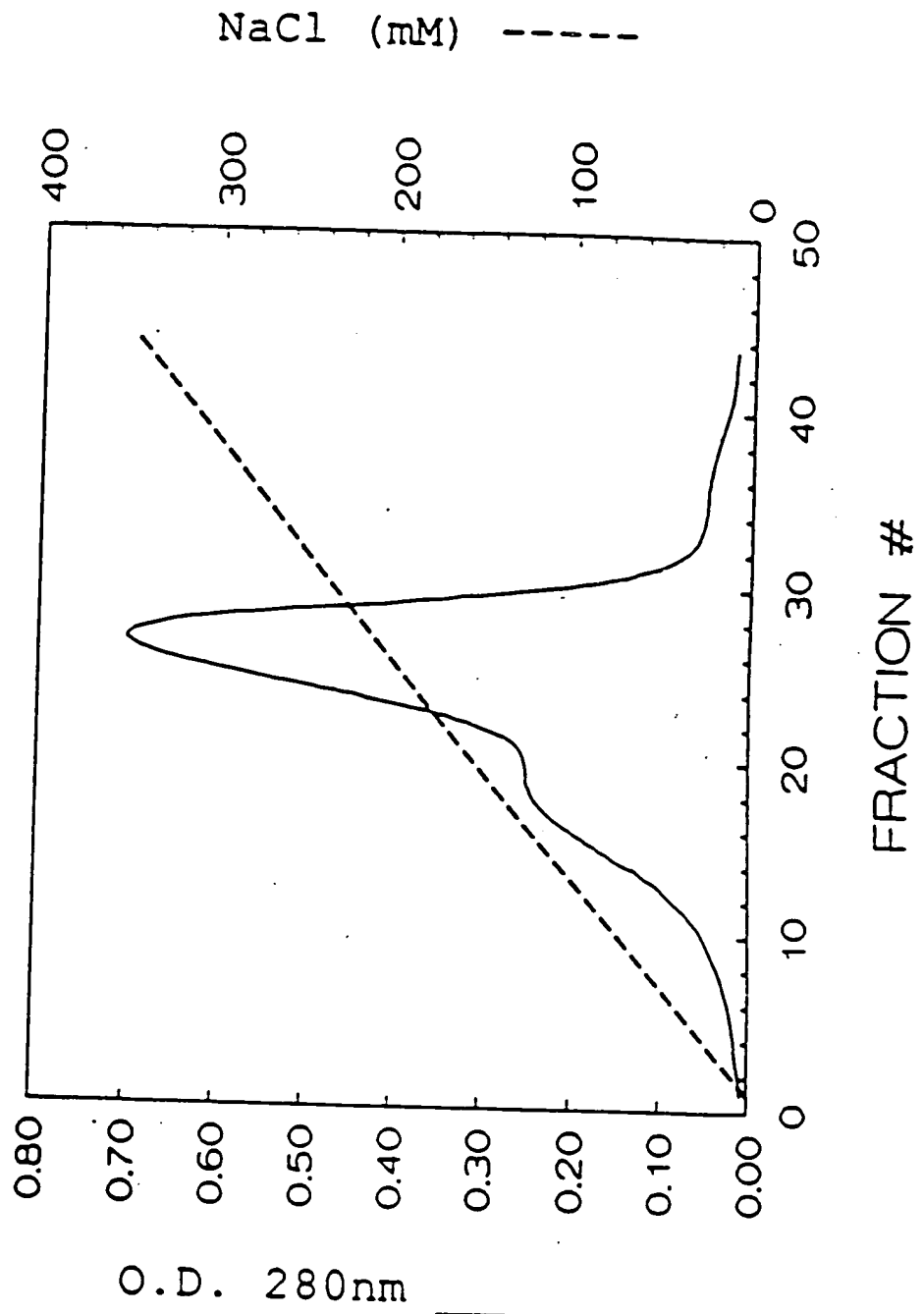


FIG. 34A

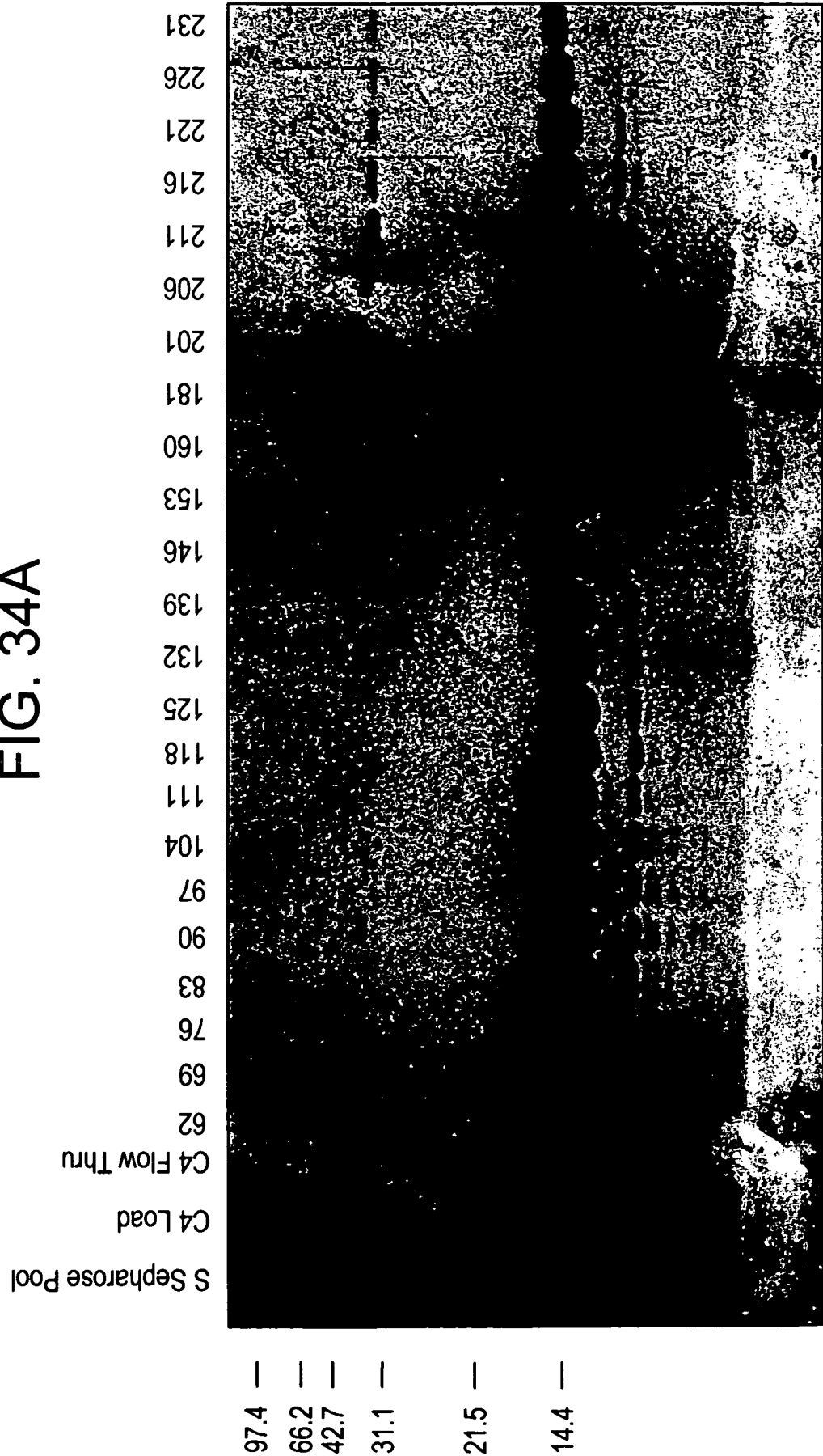
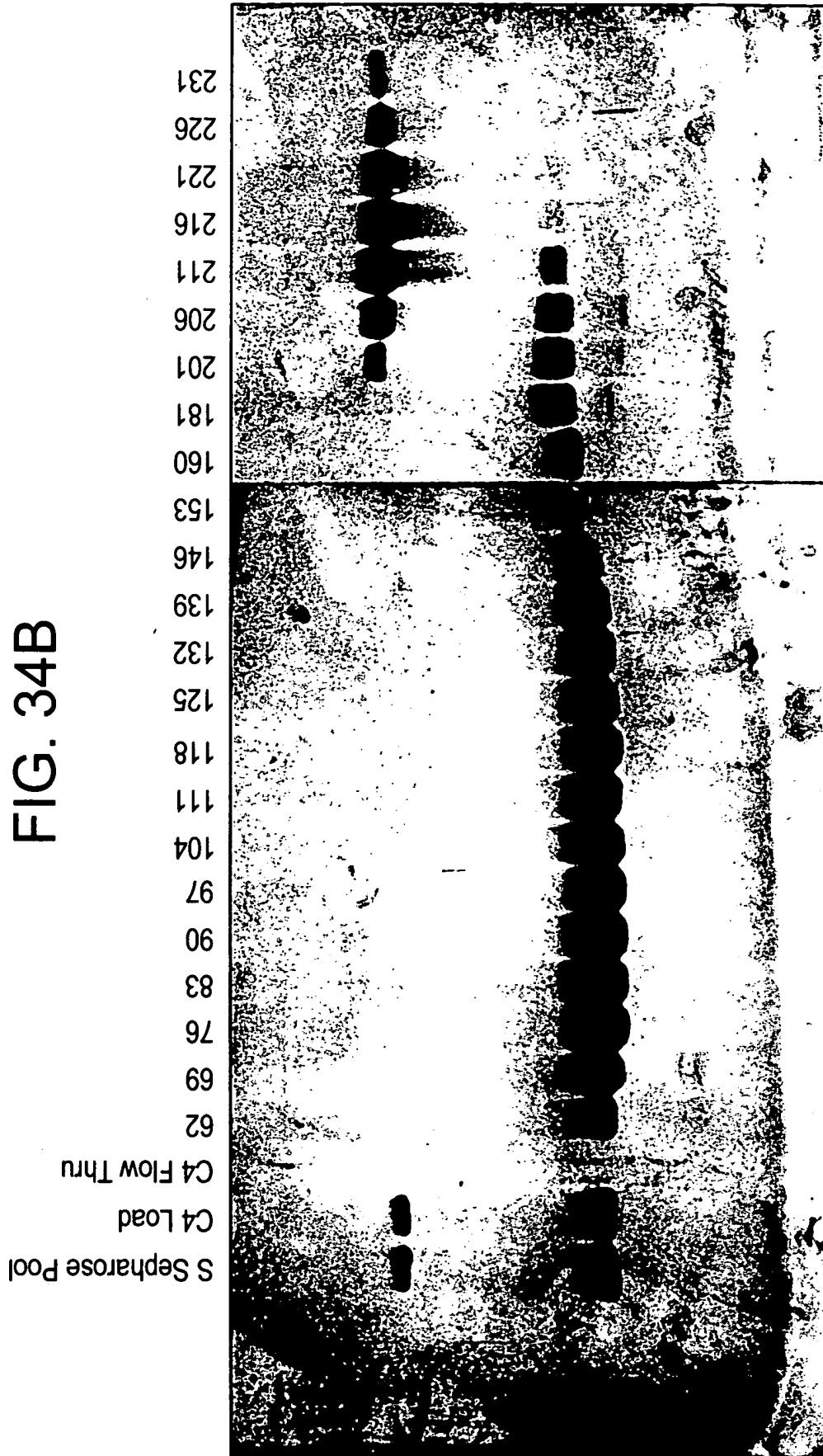
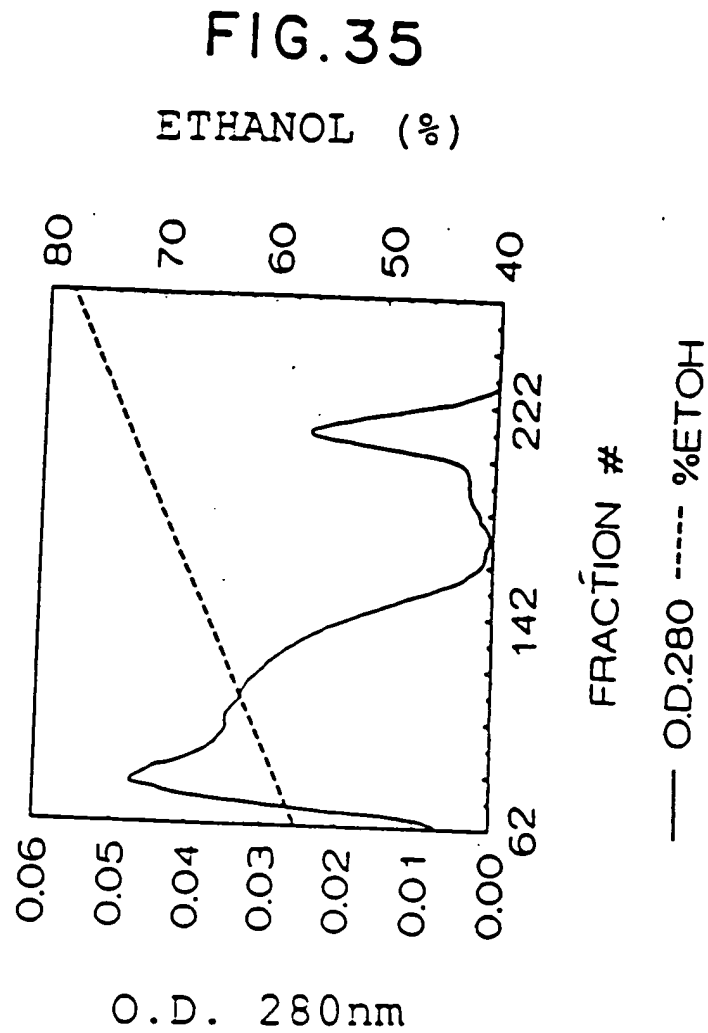
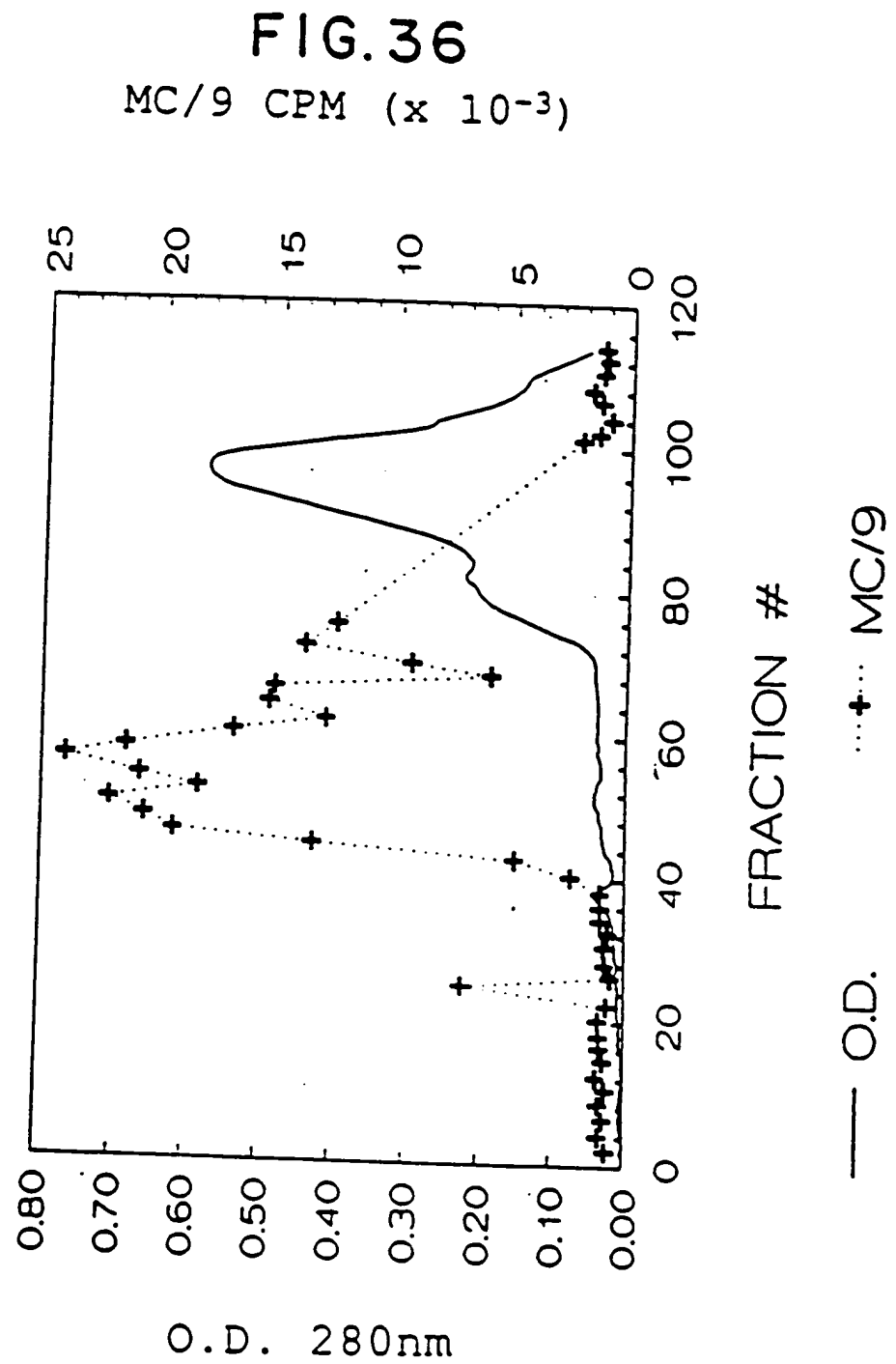


FIG. 34B







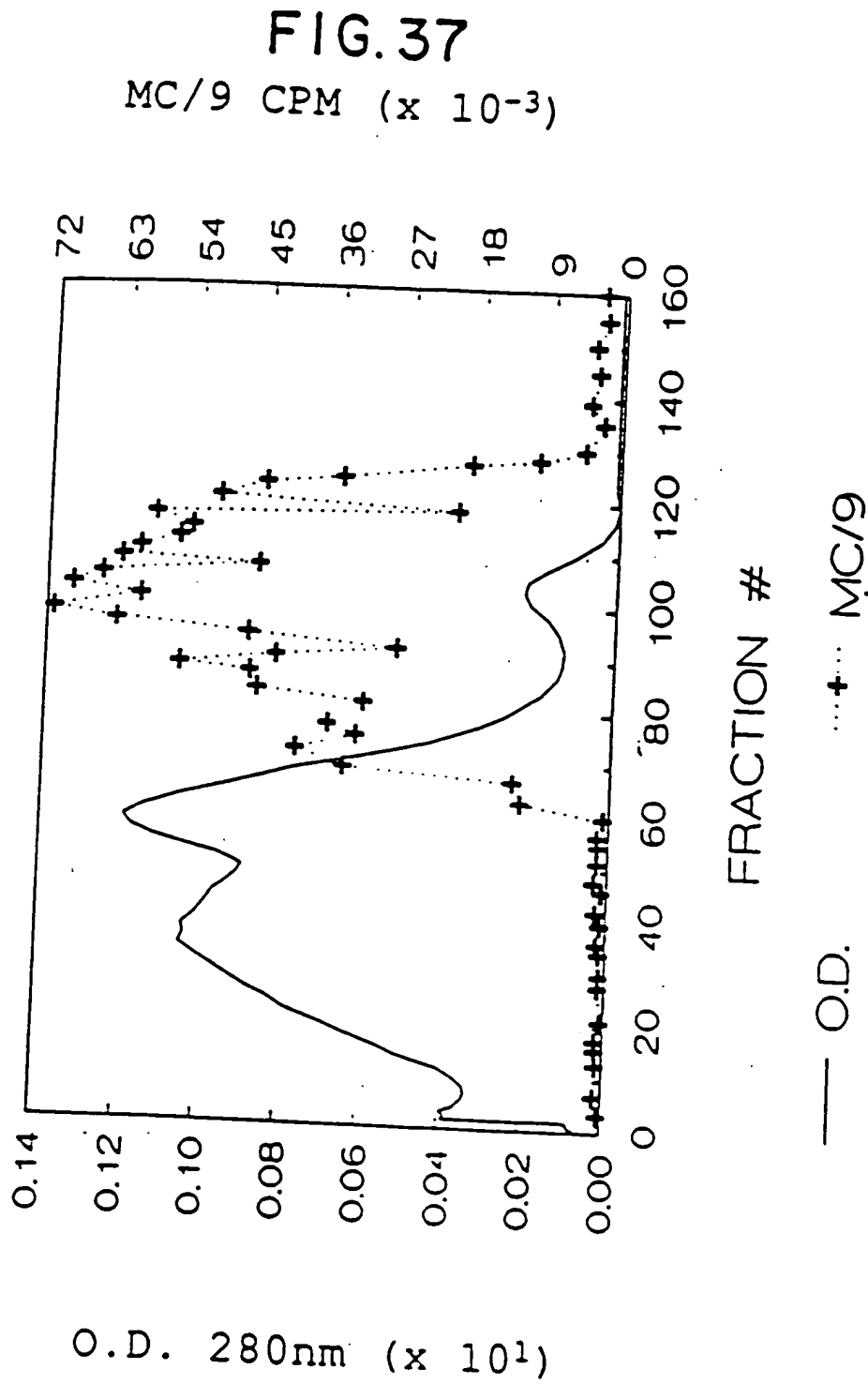


FIG. 38

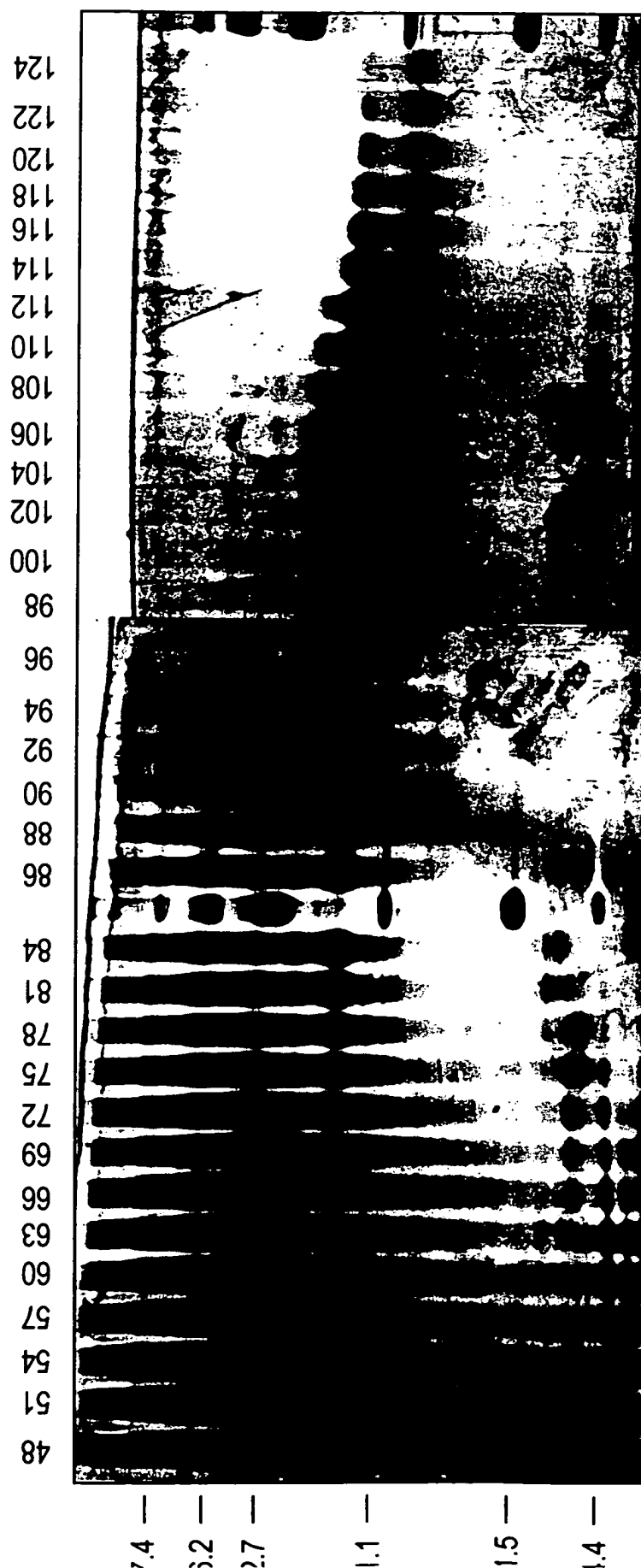


FIG. 39

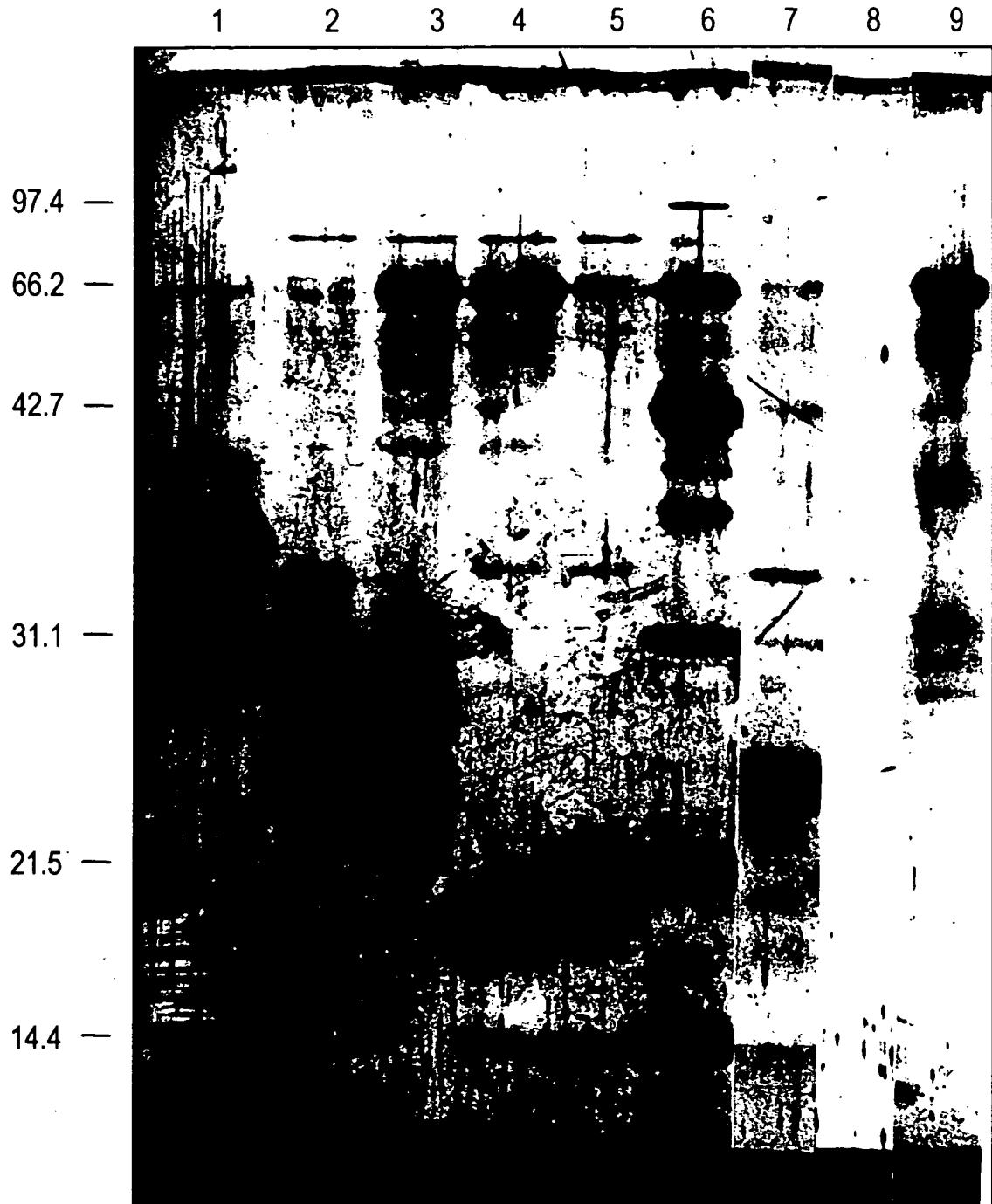


FIG. 40A

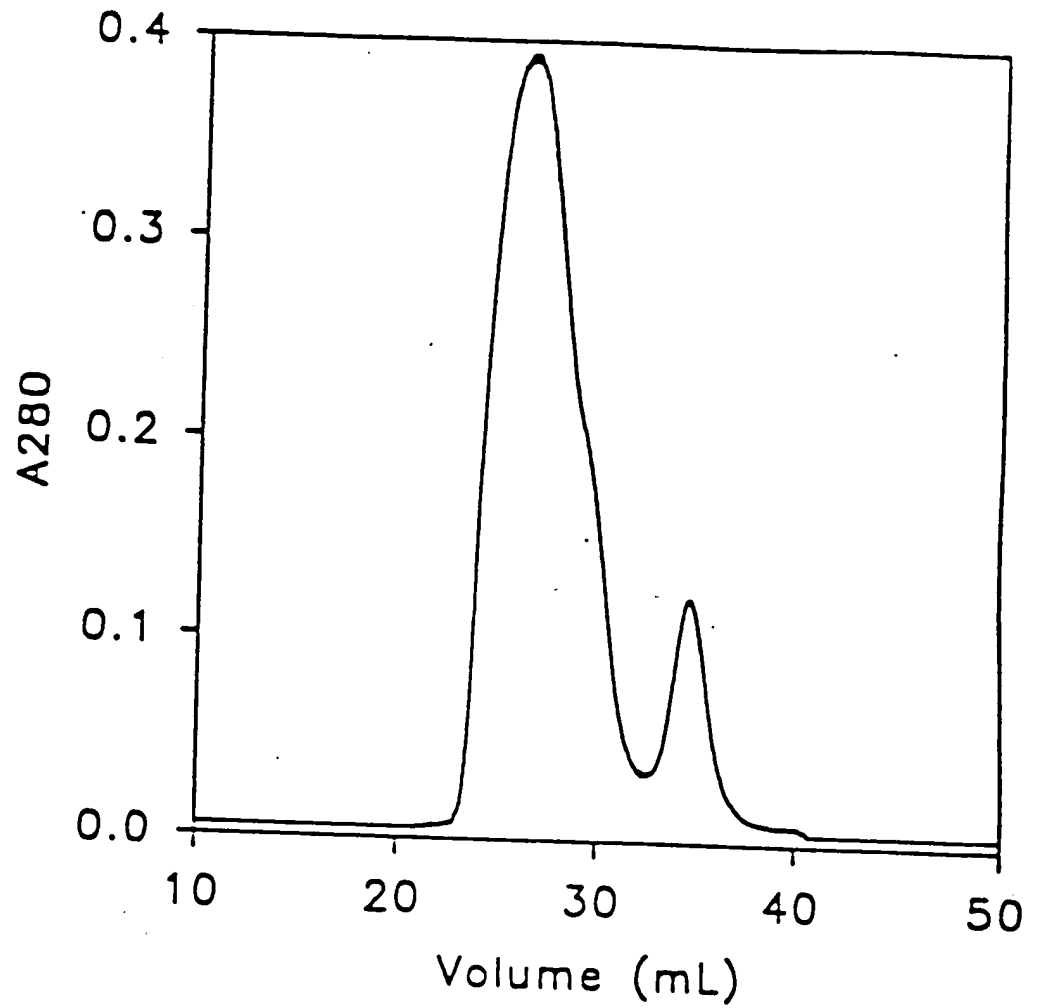


FIG. 40B

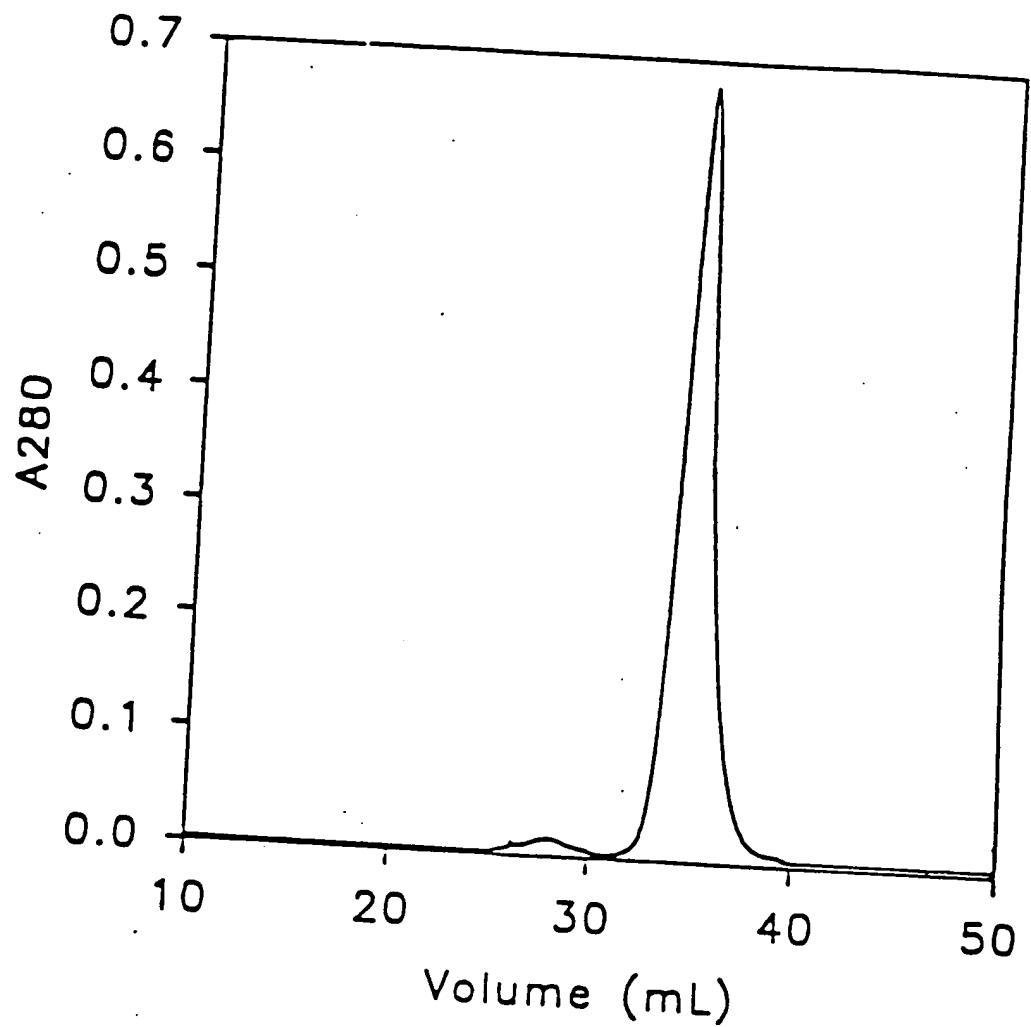


FIG. 41

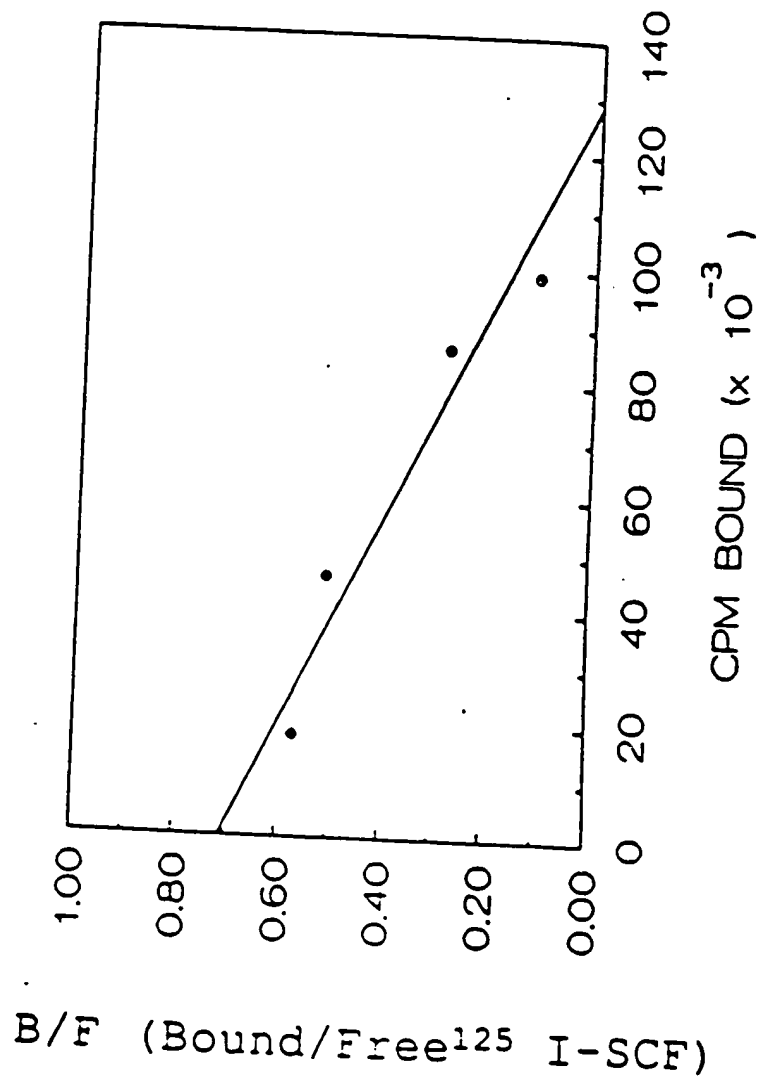


FIG. 42A

```
CCGCCTCGCCGCGAGACTAGAACGGCTGCGGGAAGCAGGACAGTGAGAGGCGCTGCCG 61
TCGGGGCTACCCCAATGCGTGGACTATCTGCCGCCGCTGTTTCGTGCAATATGCTGGAGCTCCA 122
GAACAGCTAAACGGAGTCGCCACACCACTGTTGTGCTGGATCGCAGCGCTGCCCTTTCCTT 183

-25      -20      1
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 228

-10      10      20
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG 273

Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala 20
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 318

Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 363

Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val 50
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 408

Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT 453

60
```

FIG. 42B

Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	80
ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT	GTG	498
Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	90
AAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT	543
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	110
AAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	588
Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	120
ACT	CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	633
Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	140
TTC	AAG	GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	678
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Thr	150
TCT	TCA	ACA	TTA	AGT	CCT	GAG	AAA	GAT	TCC	AGA	GTC	AGT	GTC	ACA	723

FIG. 42C

Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT	160	170	768
Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC	180	813	
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT	190	200	858
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA	210	903	
Gln Pro Ser Leu Thr ACA AGG GCA GCA GCA ATA ATA CAA ATT AAT GAA CAG CCA AGT CTT	220	230	948
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT	240	993	
Gln Glu Val End CAA GAA GTG TAA	248		
TTGTGGCTTGTATCAACACTGTTACTTTTCGTACATTGGC			1044

FIG. 42D

TGGTAACAGTTTCATGTTTGCTTCATAAATGAAGCAGCCTTTAAACAATTCATATTCTGTC 1104
TGGAGTGACAGACCAACATCTTTATCTGTCTTGCTACCCATGACTTTATATGGATGATTC 1164
AGAAATTGGAAACAGAAATGTTTACTGTGAAACTGGCAGCTGAATTAATCATCTATAAAGAA 1224
GAACTTGCAATGGAGCAGGACTCTATTTTAAGGACTGCGGGGACTTGGGTCTCATTTAGAAC 1284
TTGCAGCTGATGTTGGAAGAGAAAGCACCGTGTCTCAGACTGCATGTACCATTTGCATGGC 1344
TCCAGAAATGCTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCCAG 1404

FIG. 43

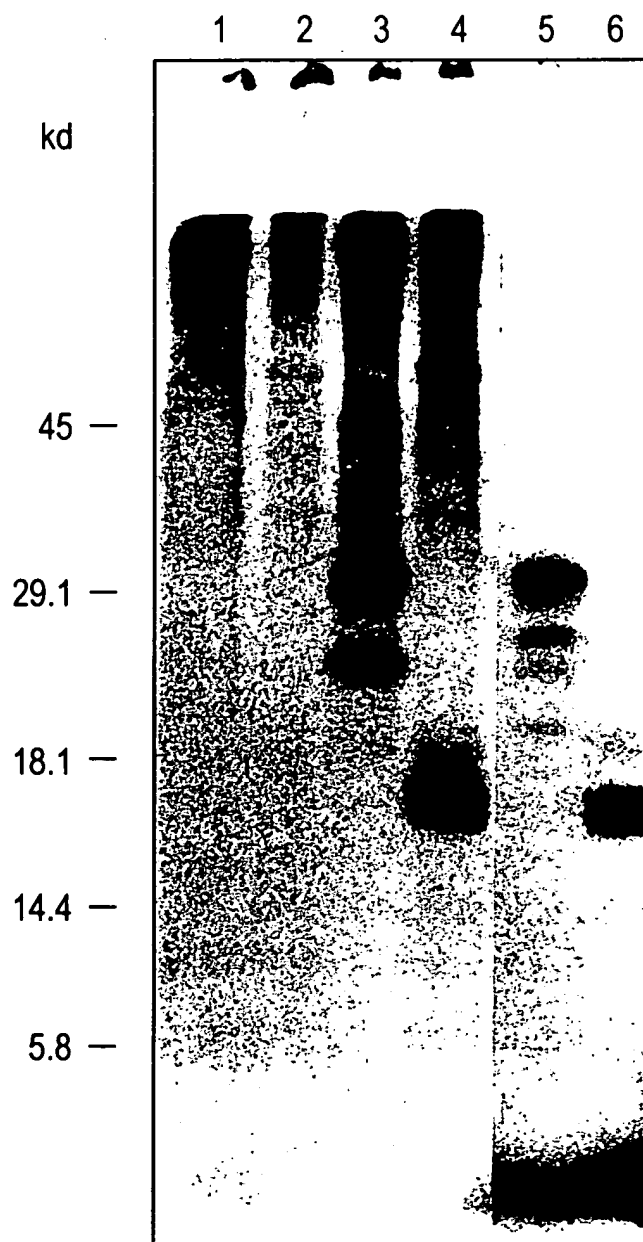


FIG. 44A

```

AGCAGGGACAGTGGAGAGGGCGCTGCGCTC 30
GGGCTACCCAAATGCGTGGACTATCTGCCCGCGCTGTTTCGTGCAATATGCTGGAGCTCCAG 90
AACAGCTAAACGGAGTCGCCACACCACTGTTGTGTGGATCGCAGCGCTGCCTTTCCCTT 150
-25
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 195
-10
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC CTC GTC AAA ACT GAA GGG ATC TGC AGG 240
10
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 285
30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 330
40
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 375
50
```

FIG. 44B

Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	420
CAA	TTG	TCA	GAC	AGC	TTG	ACT	GAT	CTT	CTG	GAC	AAG	TTT	TCA	AAT	
Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	80
ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT	GTG	465
Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	510
AAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT	
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	110
AAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	555
Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	600
ACT	CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	
Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	140
TTC	AAG	GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	645
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Gly	Lys	Ala	Lys	Asn	Pro	Pro	690
TCT	TCA	ACA	TTA	AGT	CCT	GAG	AAA	GGG	AAG	GCC	AAA	AAT	CCC	CCT	

FIG. 44C

```

160      Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu      170
      GGA GAC TCC AGC CTA CAC CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG      735

180      Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
      TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG      780

190      Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile      200
      AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT      825

210      Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Glu Glu Lys Glu Arg
      AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA      870

220      Glu Phe Gln Glu Val End
      GAG TTT CAA GAA GTG TAA      TTGTGGCTTGTATCAACACTGTTACTTTCGTA      920

      CATTGGCTGGTAACAGTTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAATTCATA      980
      TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTCTTGTGCTACCCATGACTTTATATGG      1040
      ATGATTCAGAAATTGGAACAGAAATGTTTTACTGTGAAACTGGCACTGA      1088
```

FIG. 45

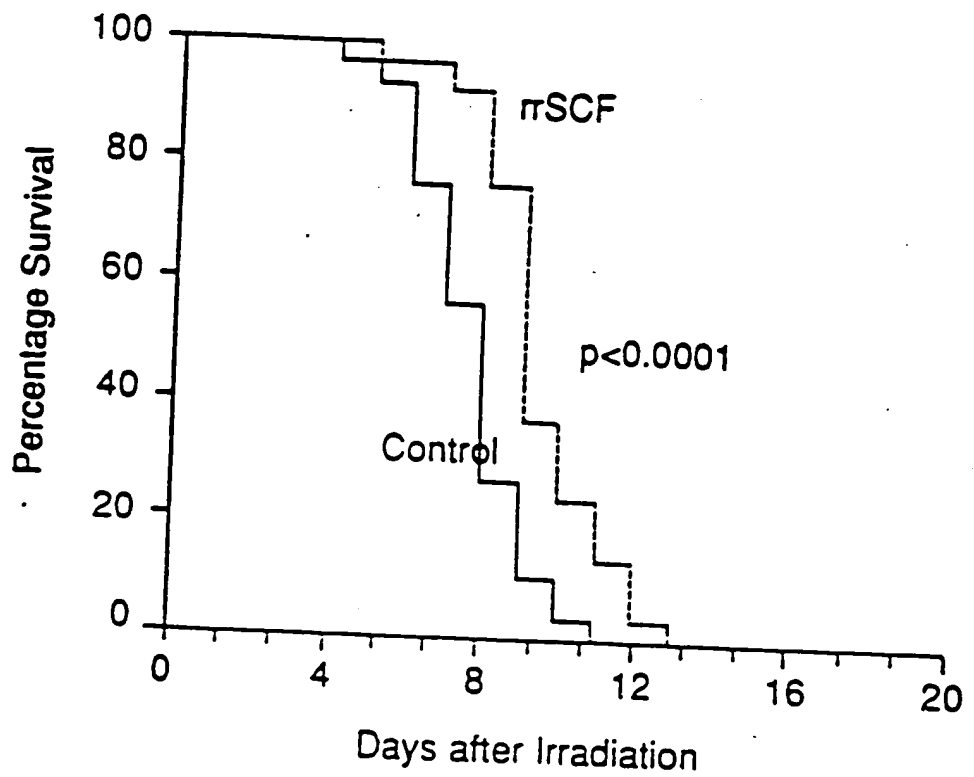
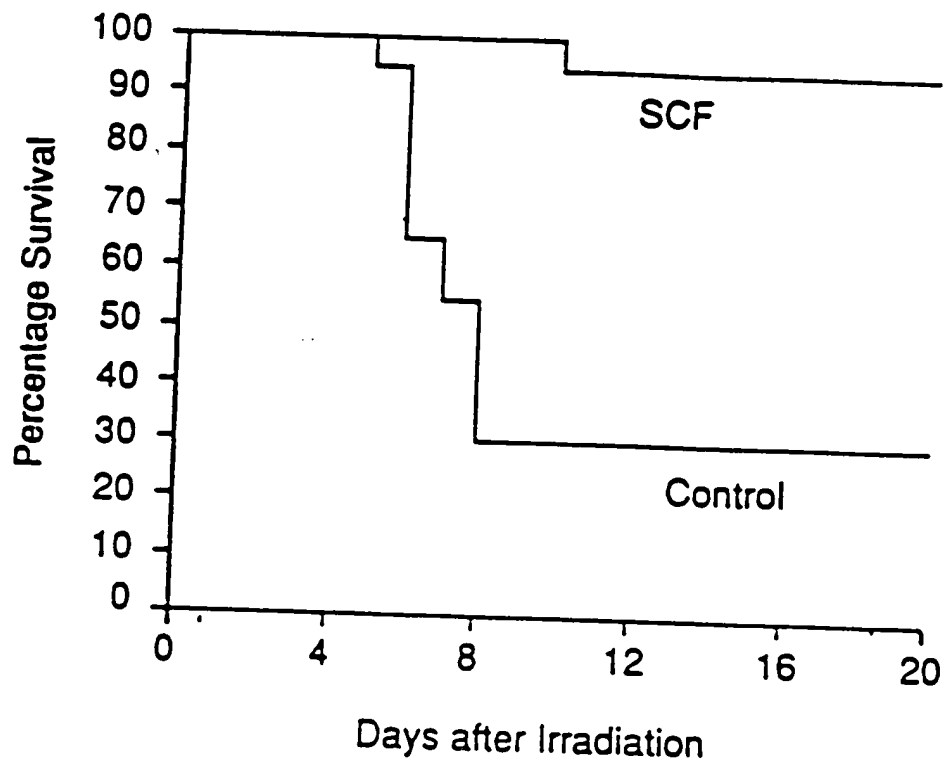
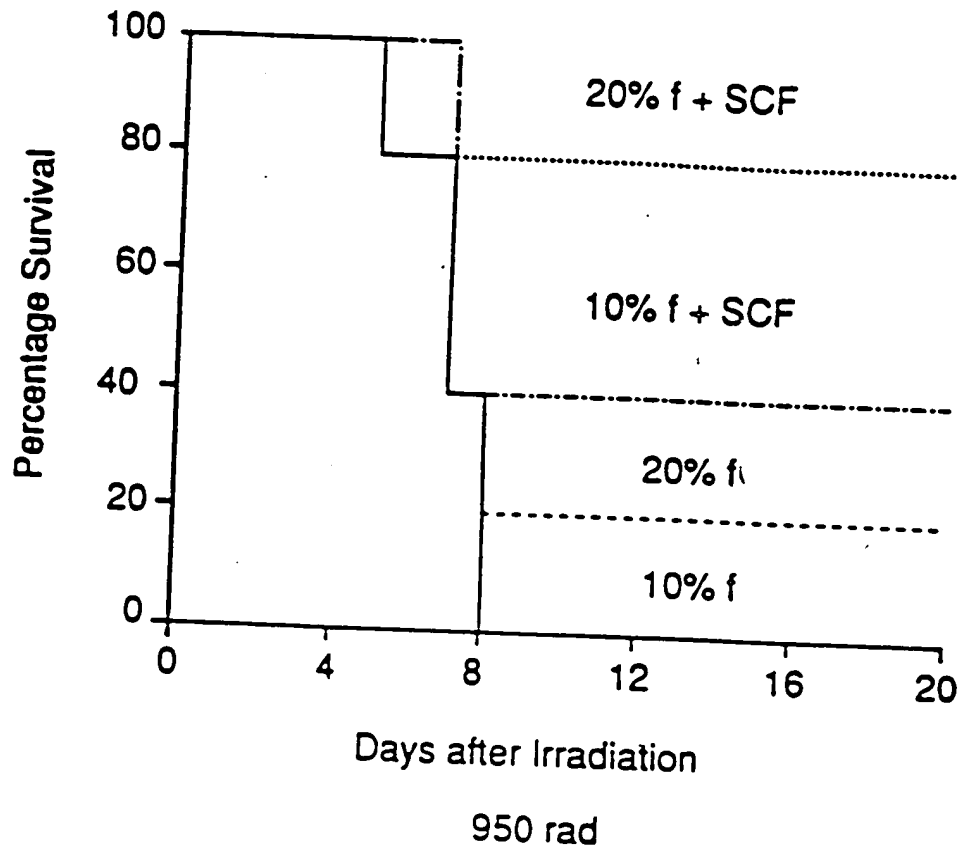


FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47



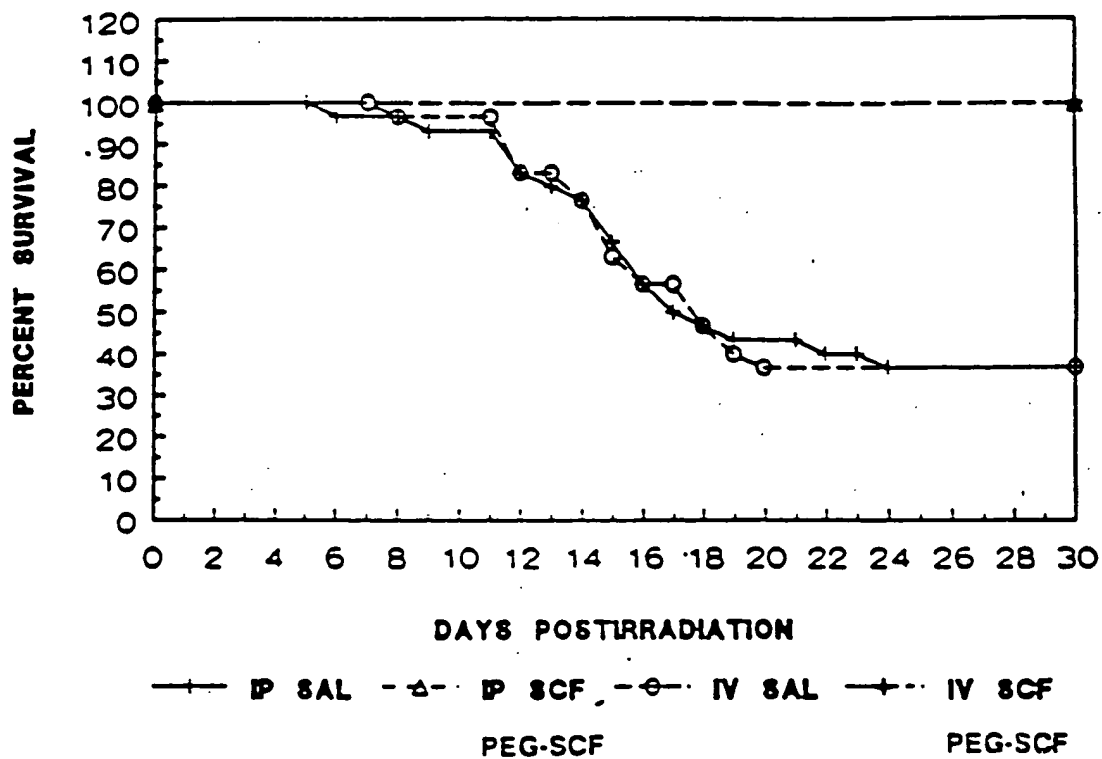


FIG. 49

SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice

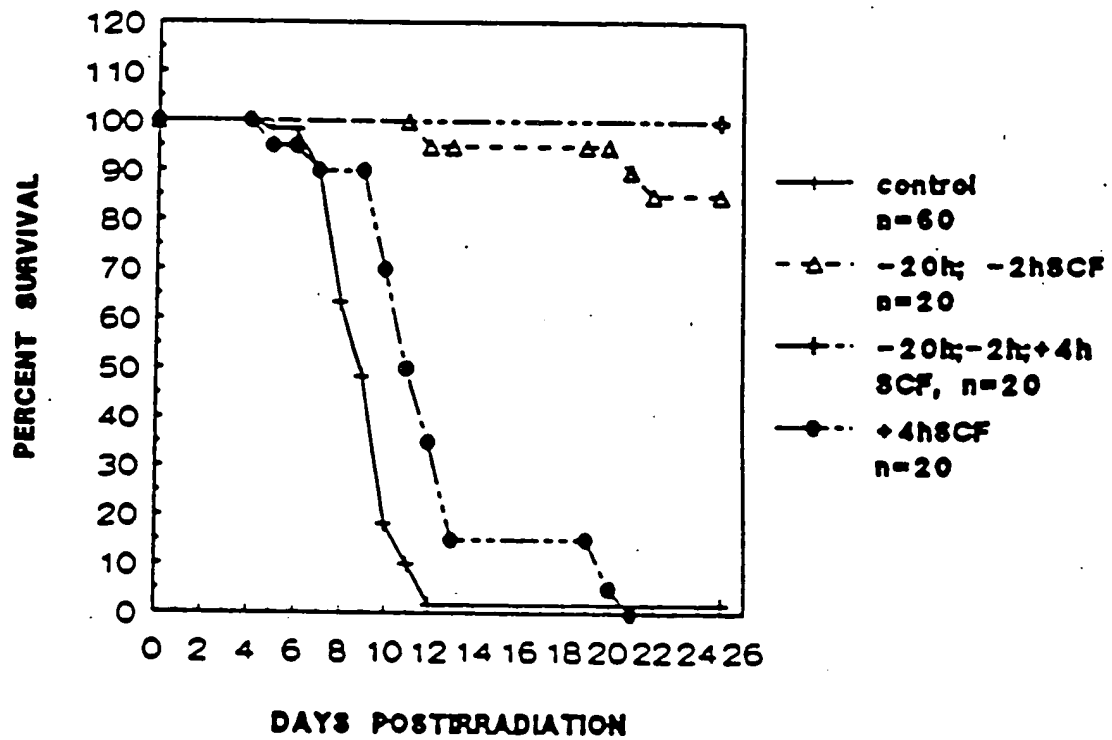


FIG. 50

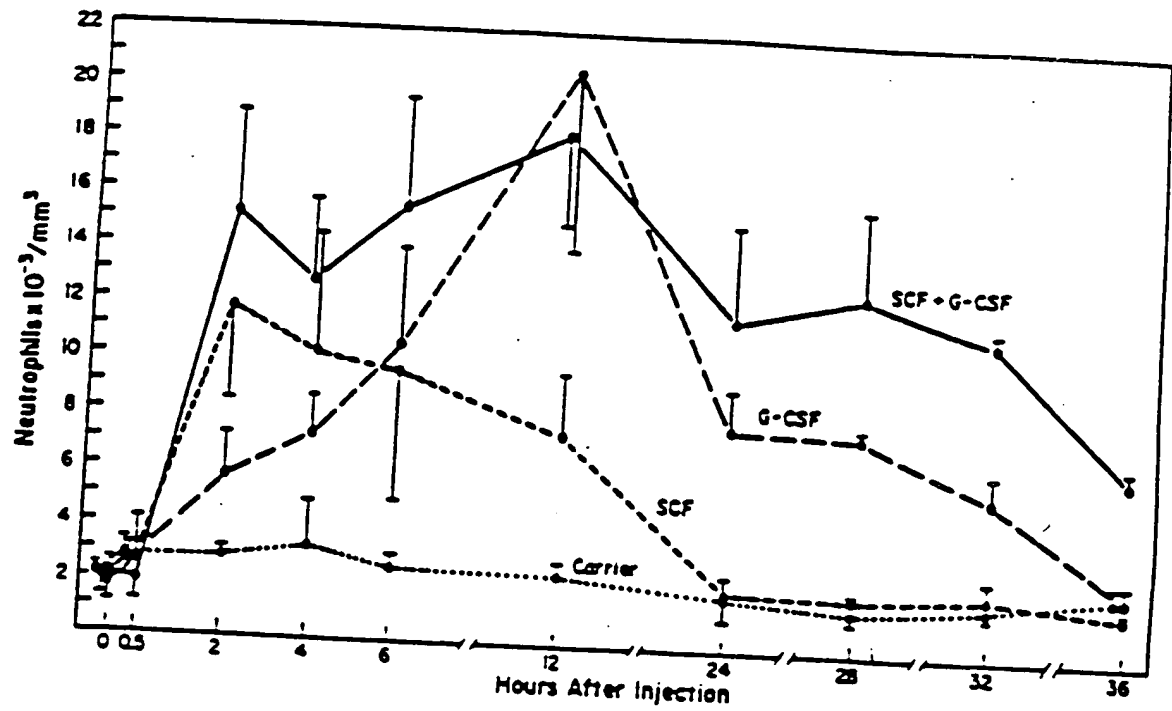


FIG. 51

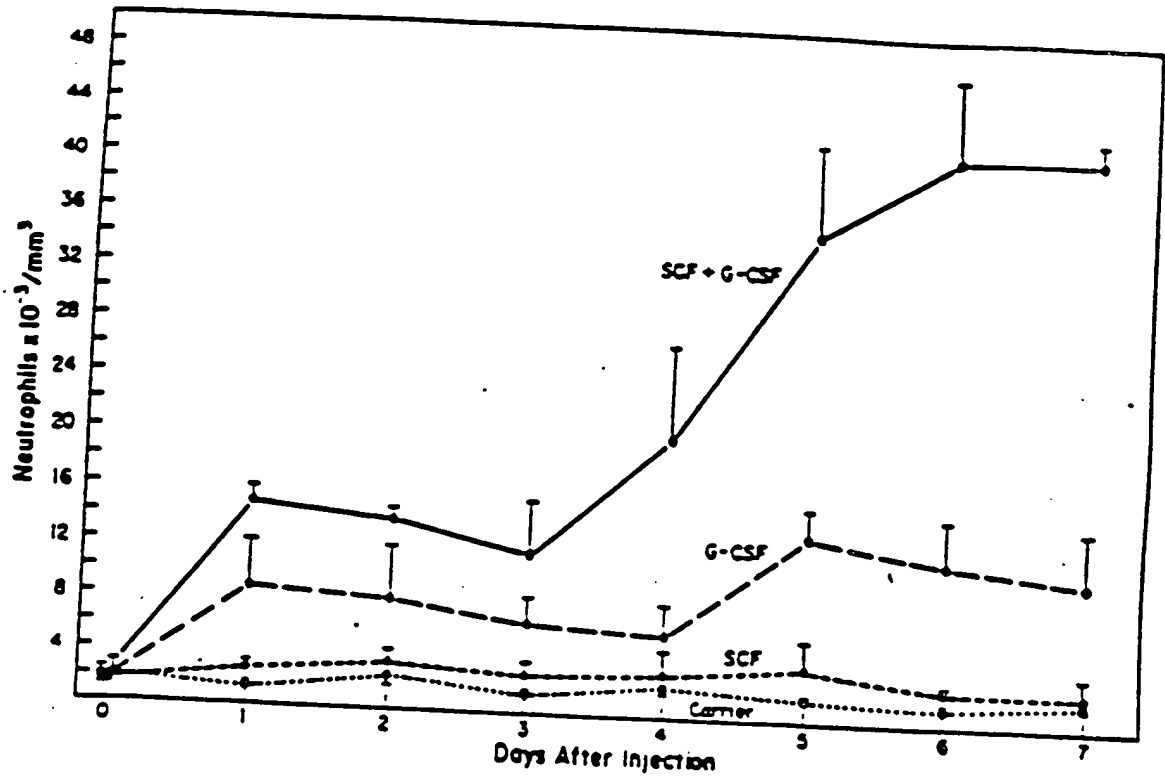


FIG. 52

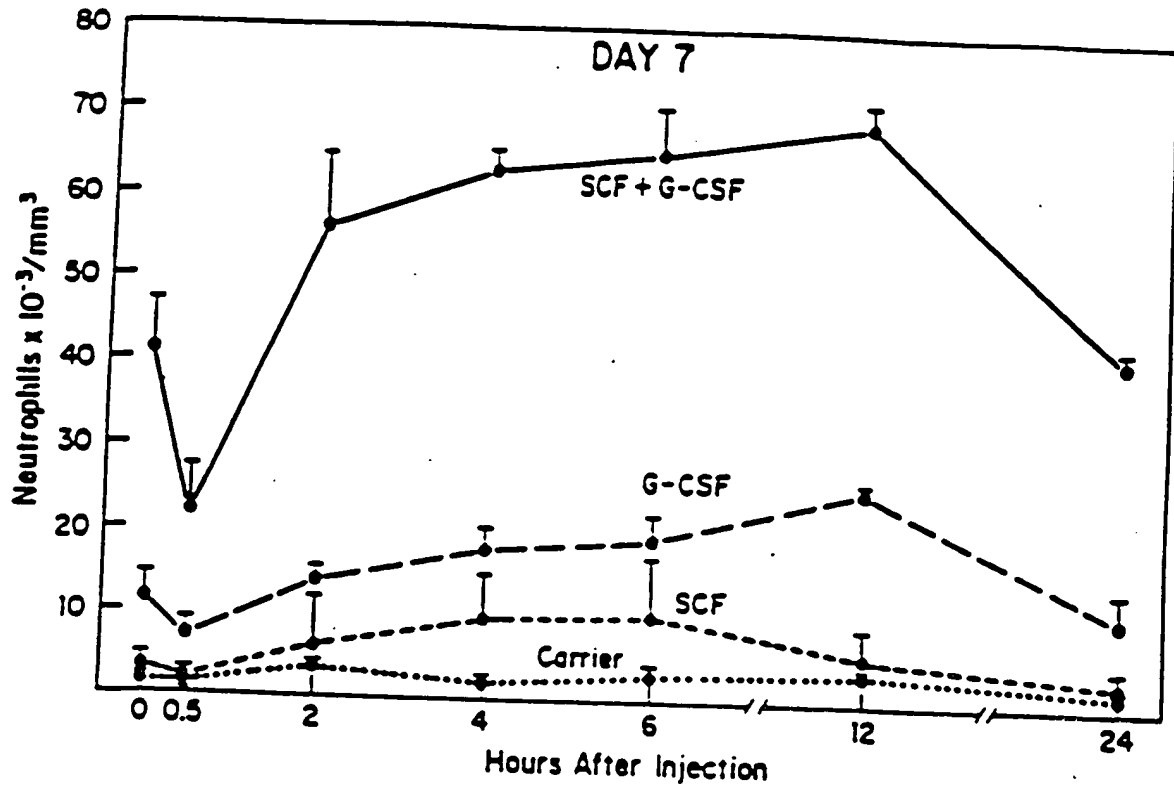


FIG. 53

in vivo Administration of SCF-Platelet Counts

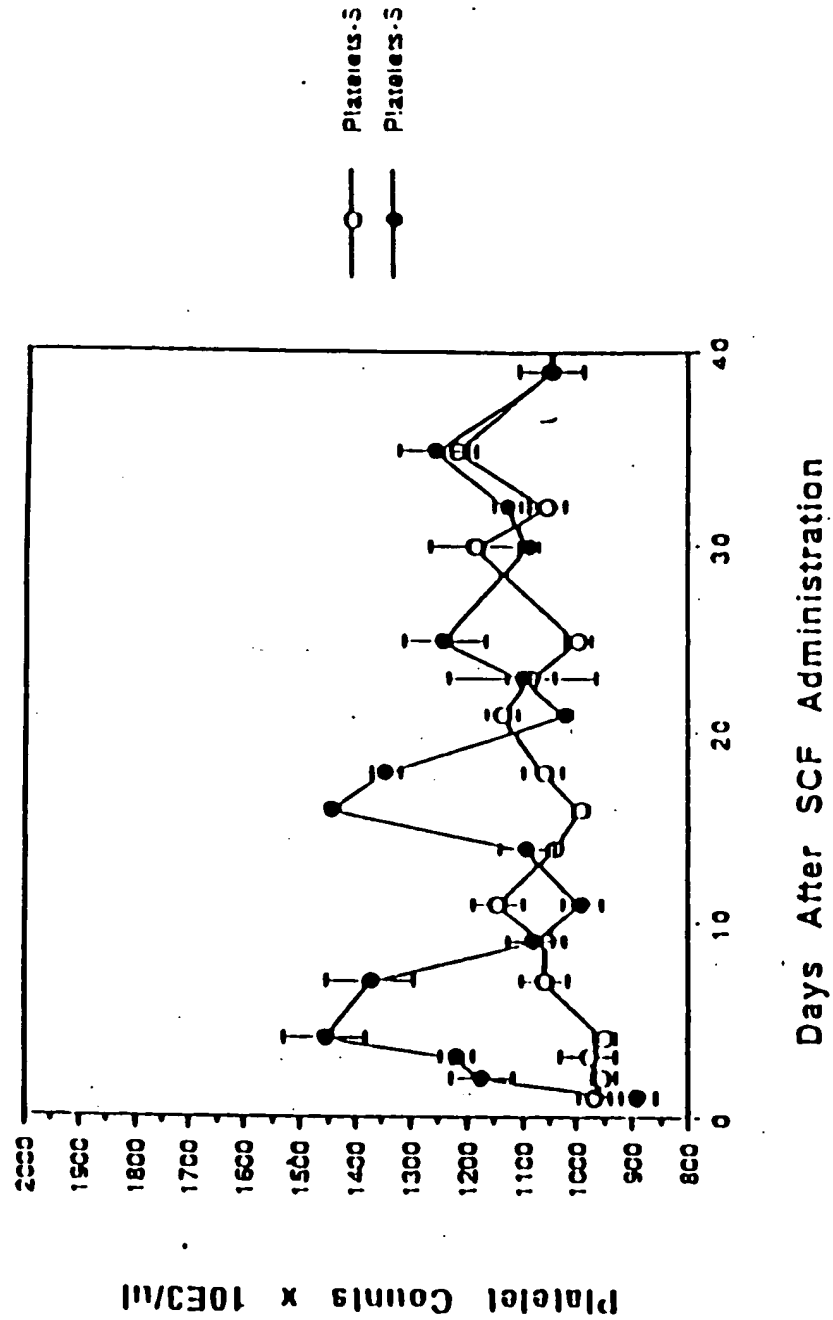


FIG. 54

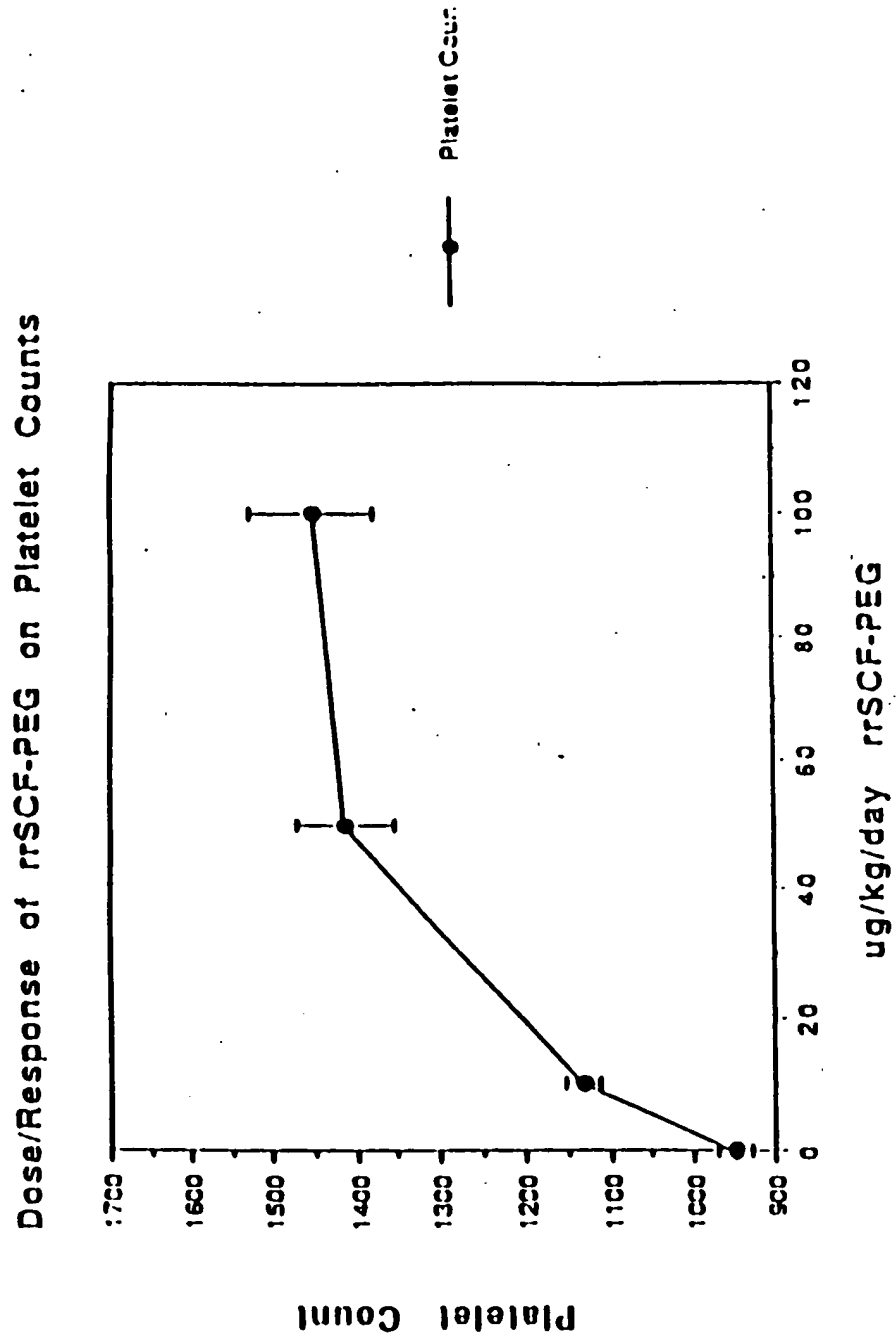


FIG. 55

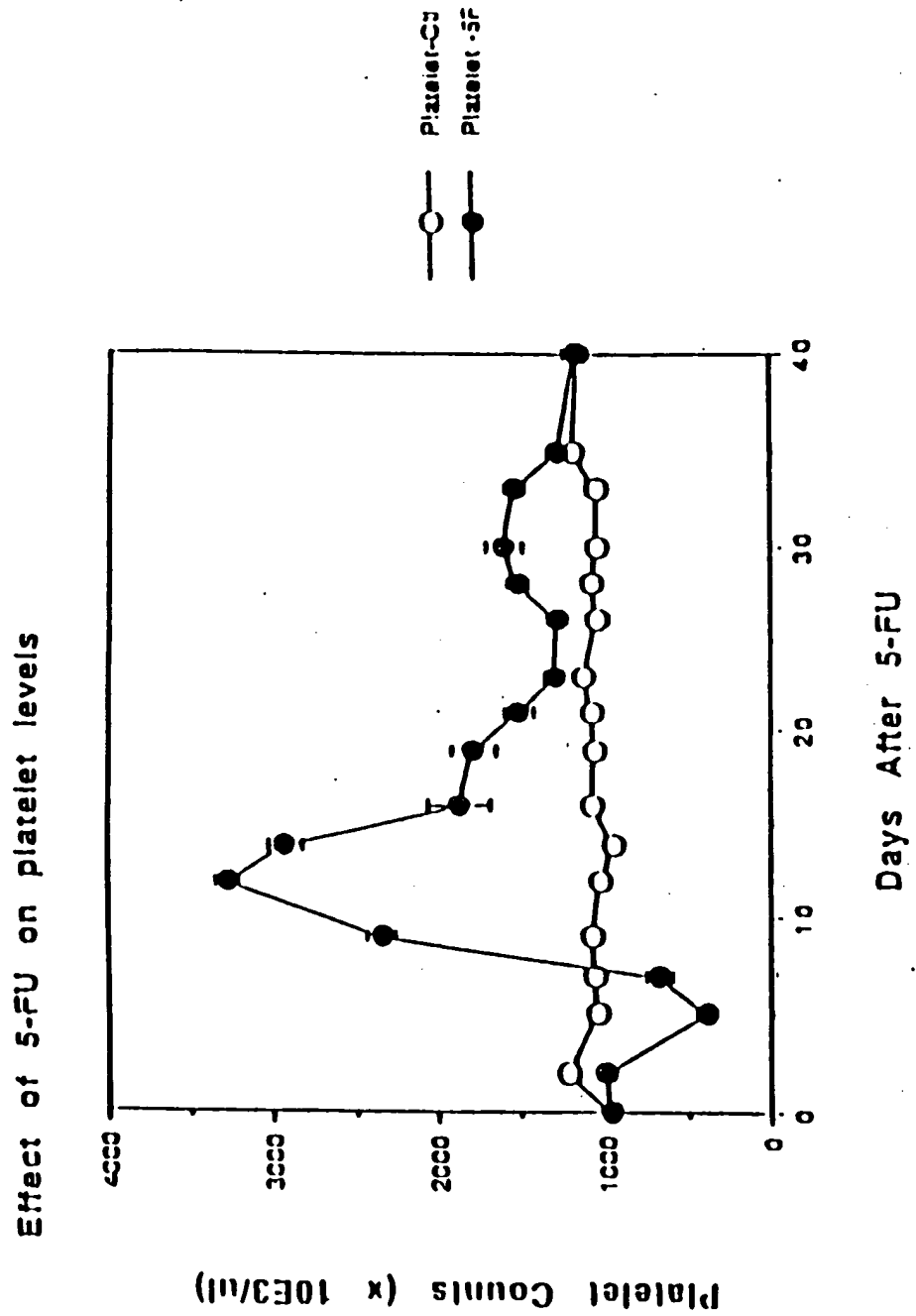
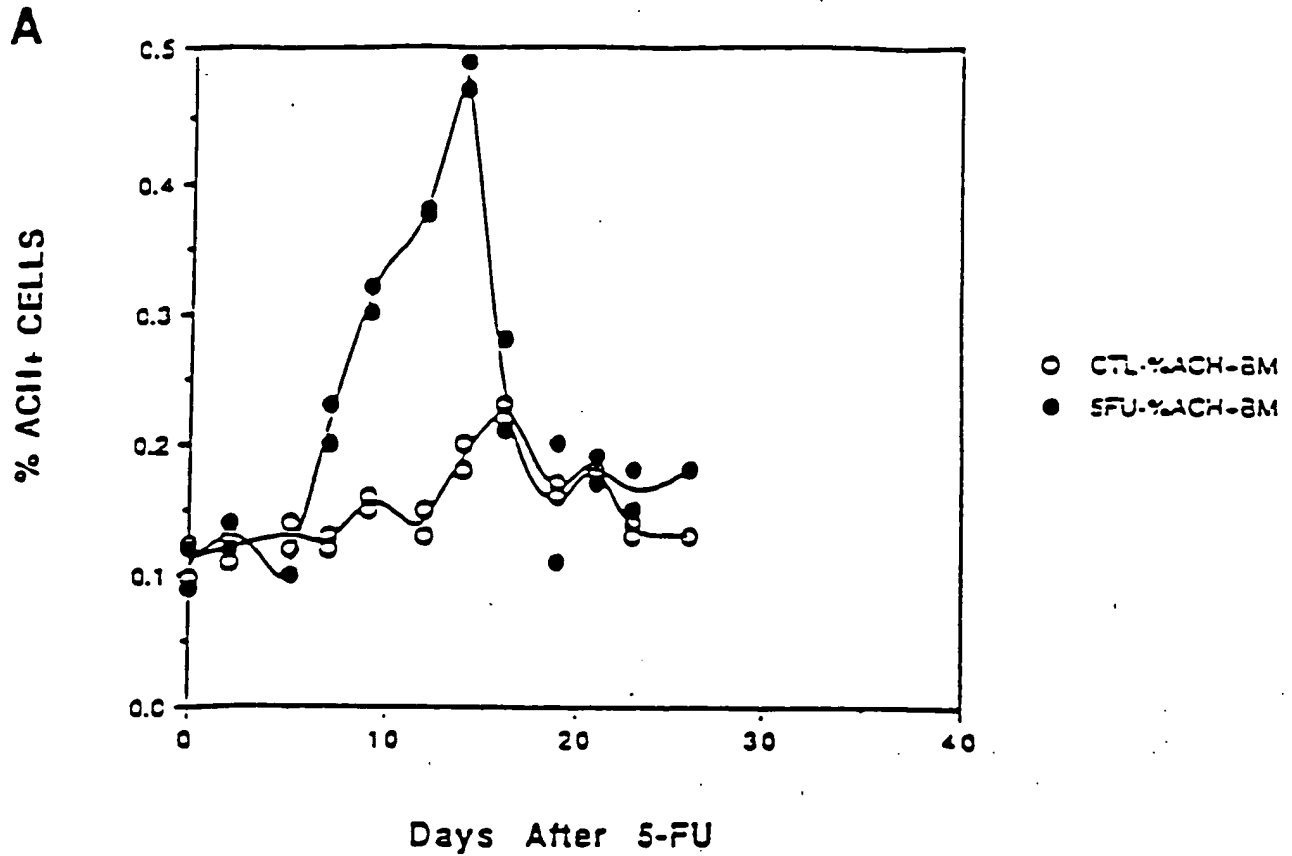


FIG. 56

5-FU Effect on ACH+ Cells in Marrow



5-FU Effect on ACH+ Cells in Spleen

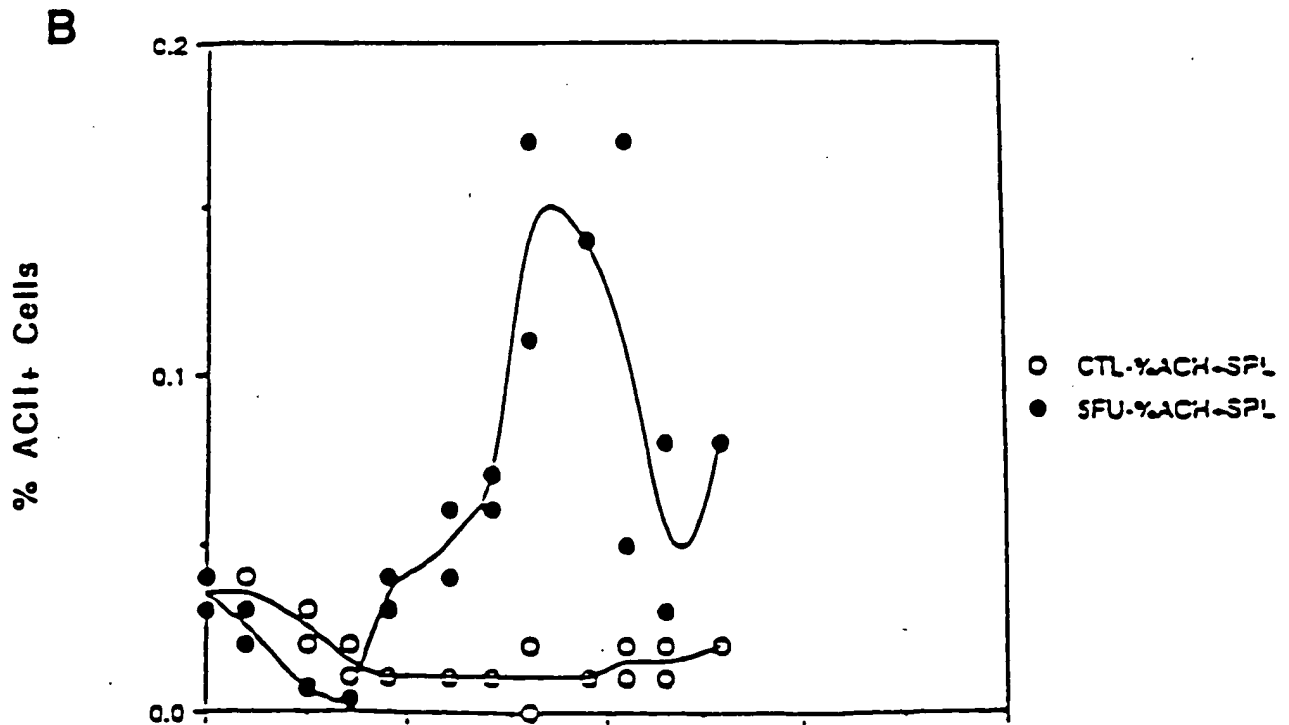


FIG. 57

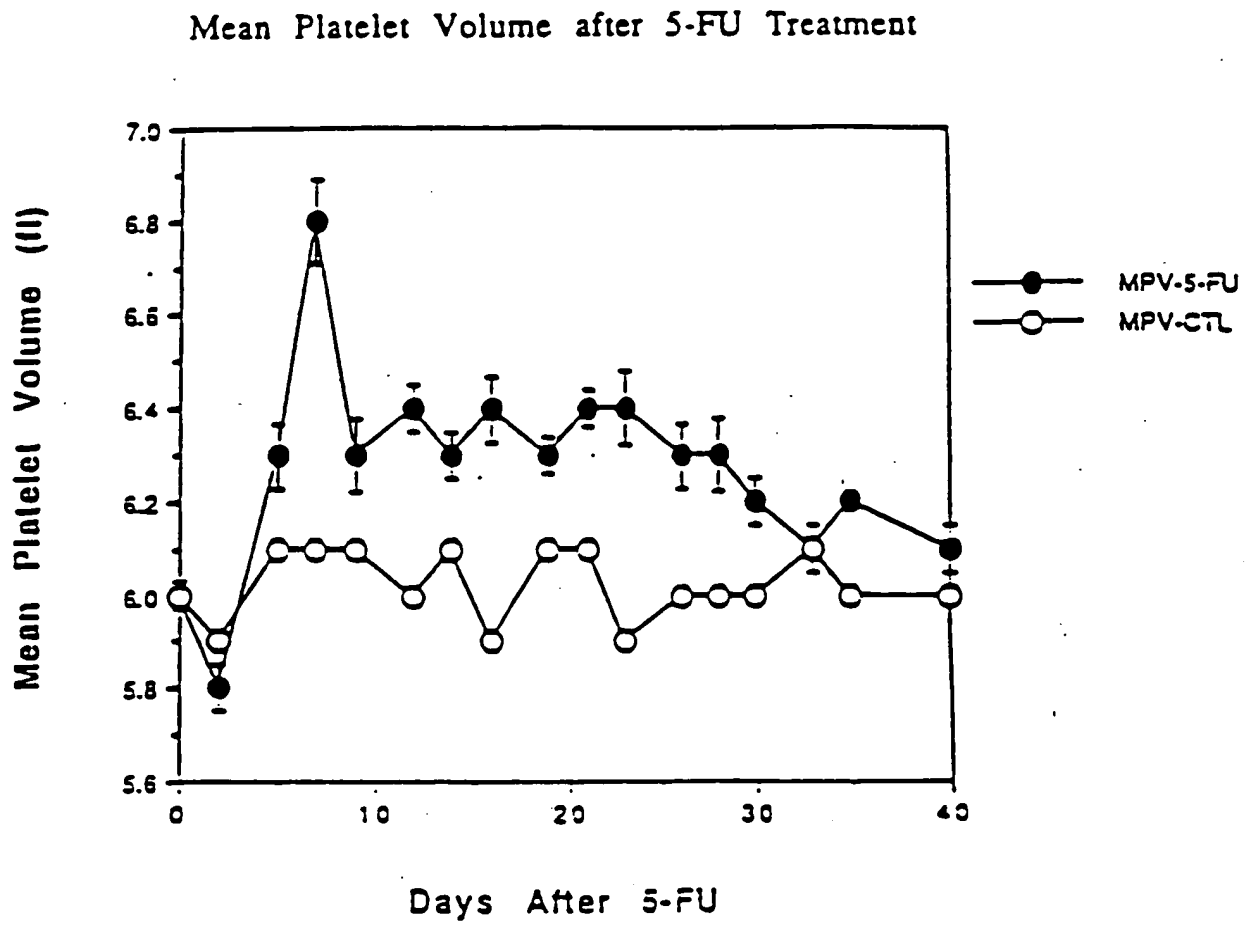


FIG. 58

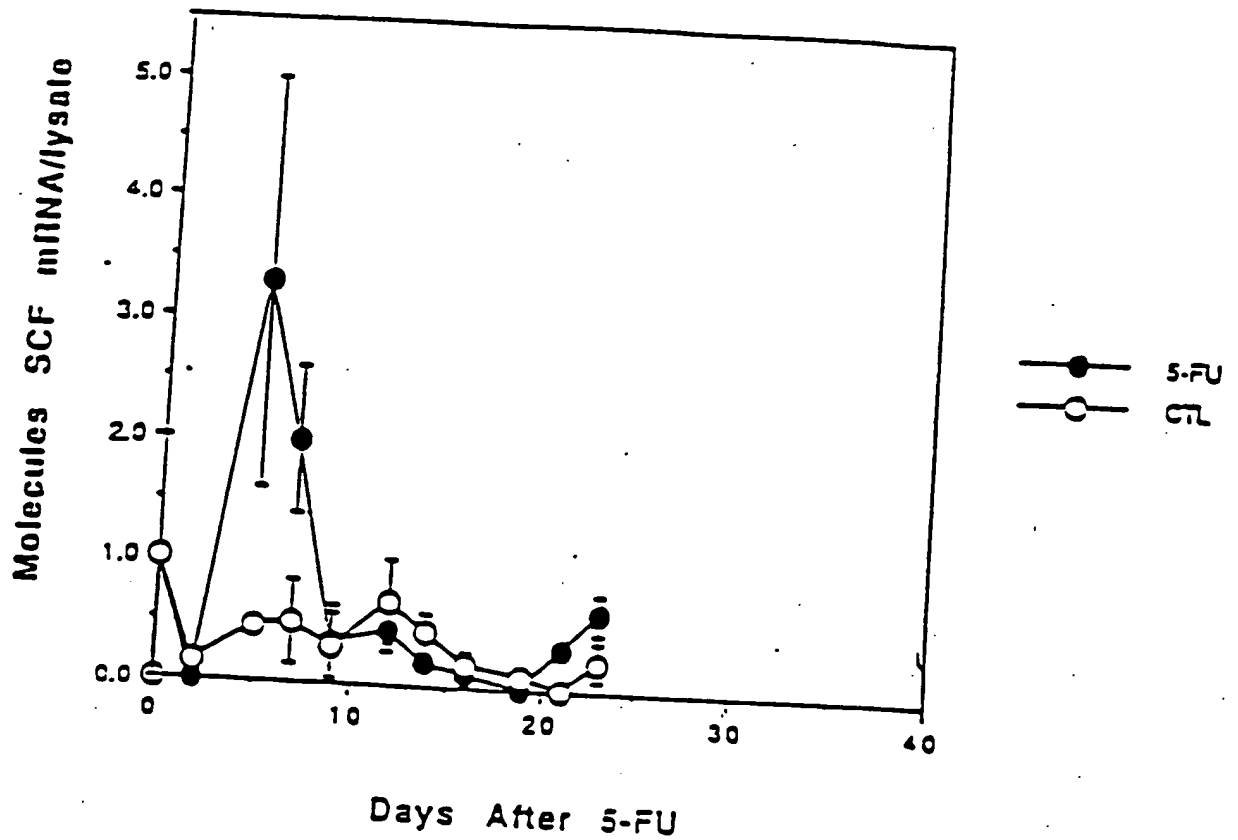


FIG. 59

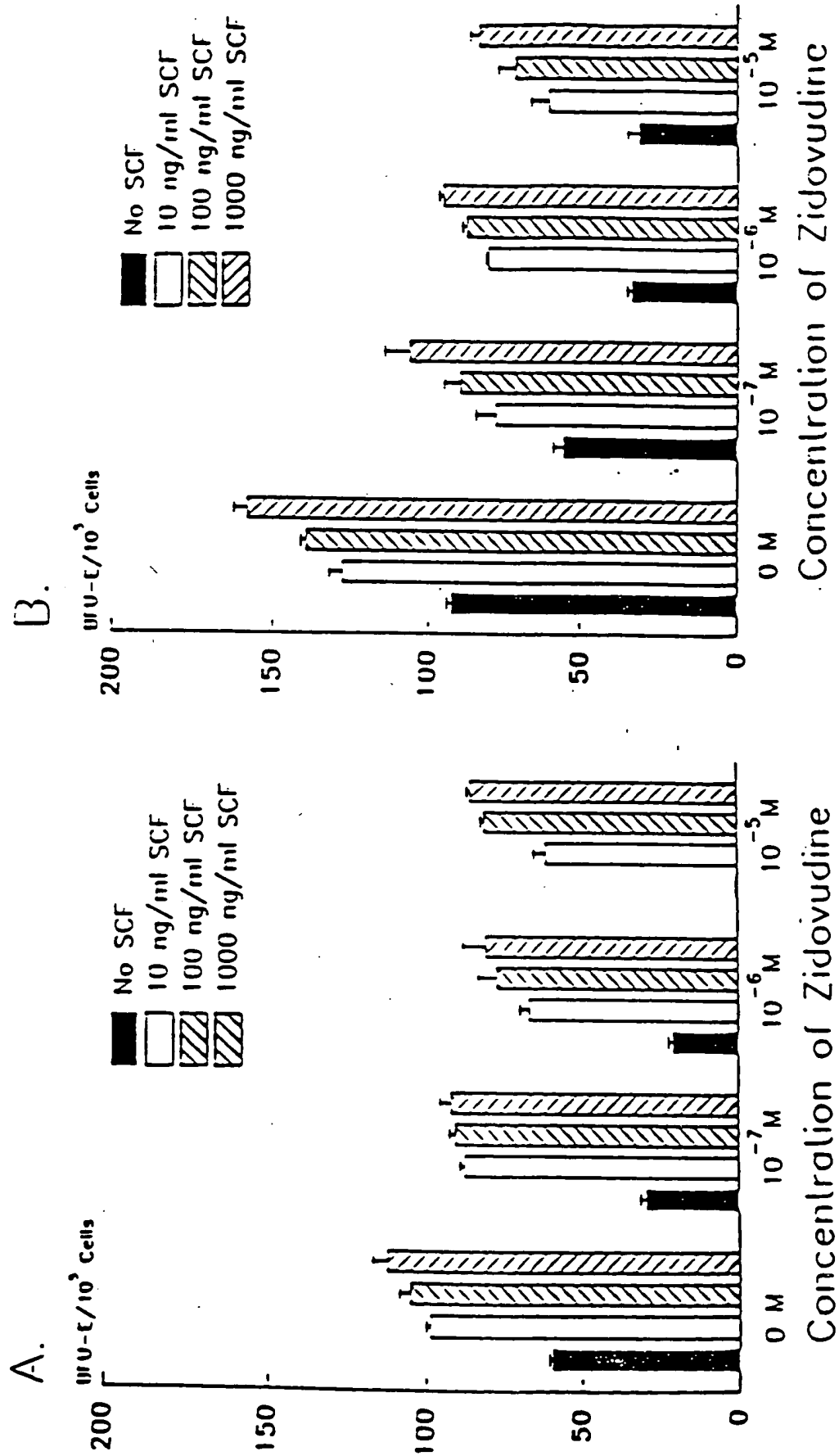


FIG. 60

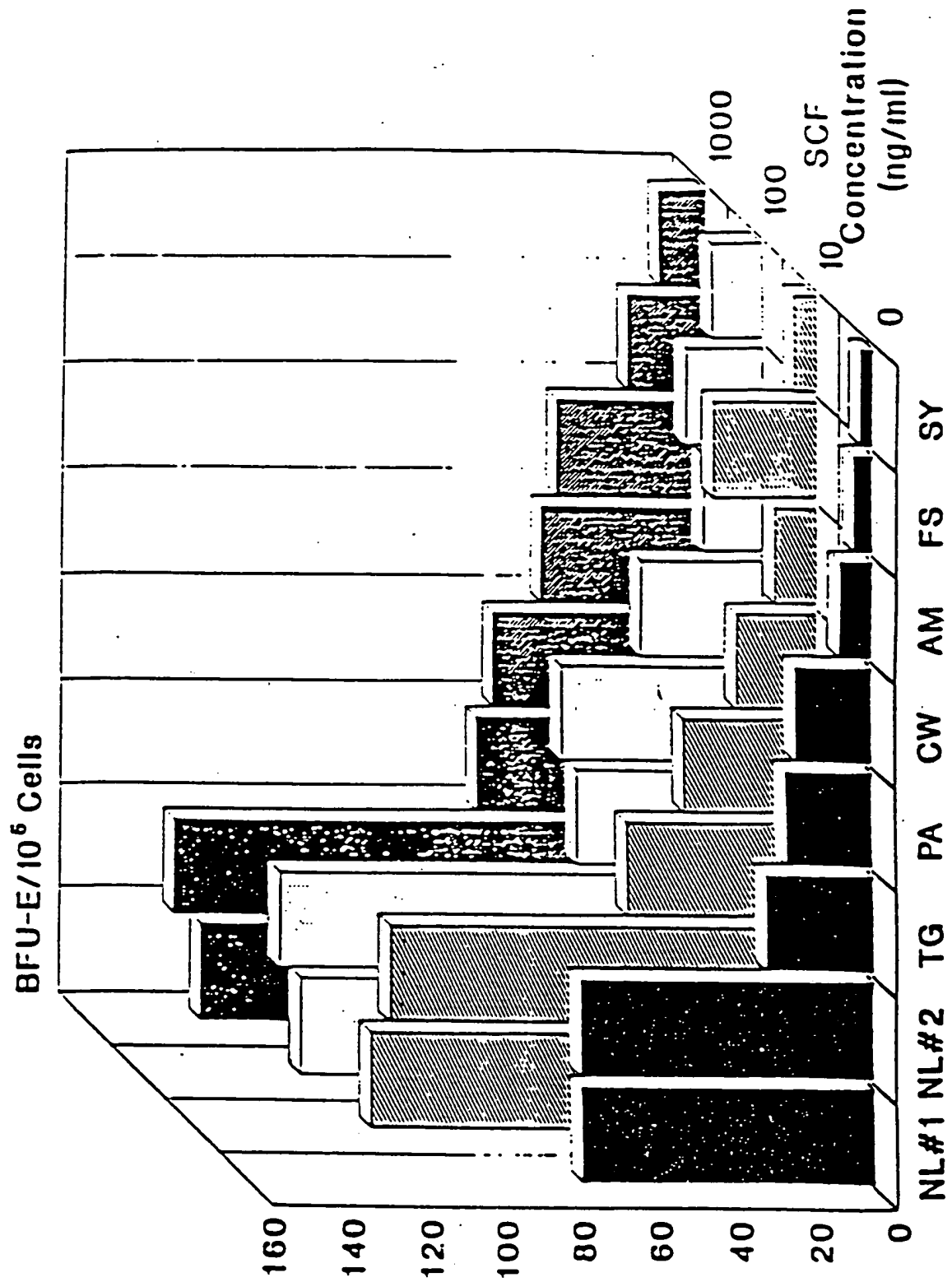


FIG. 61

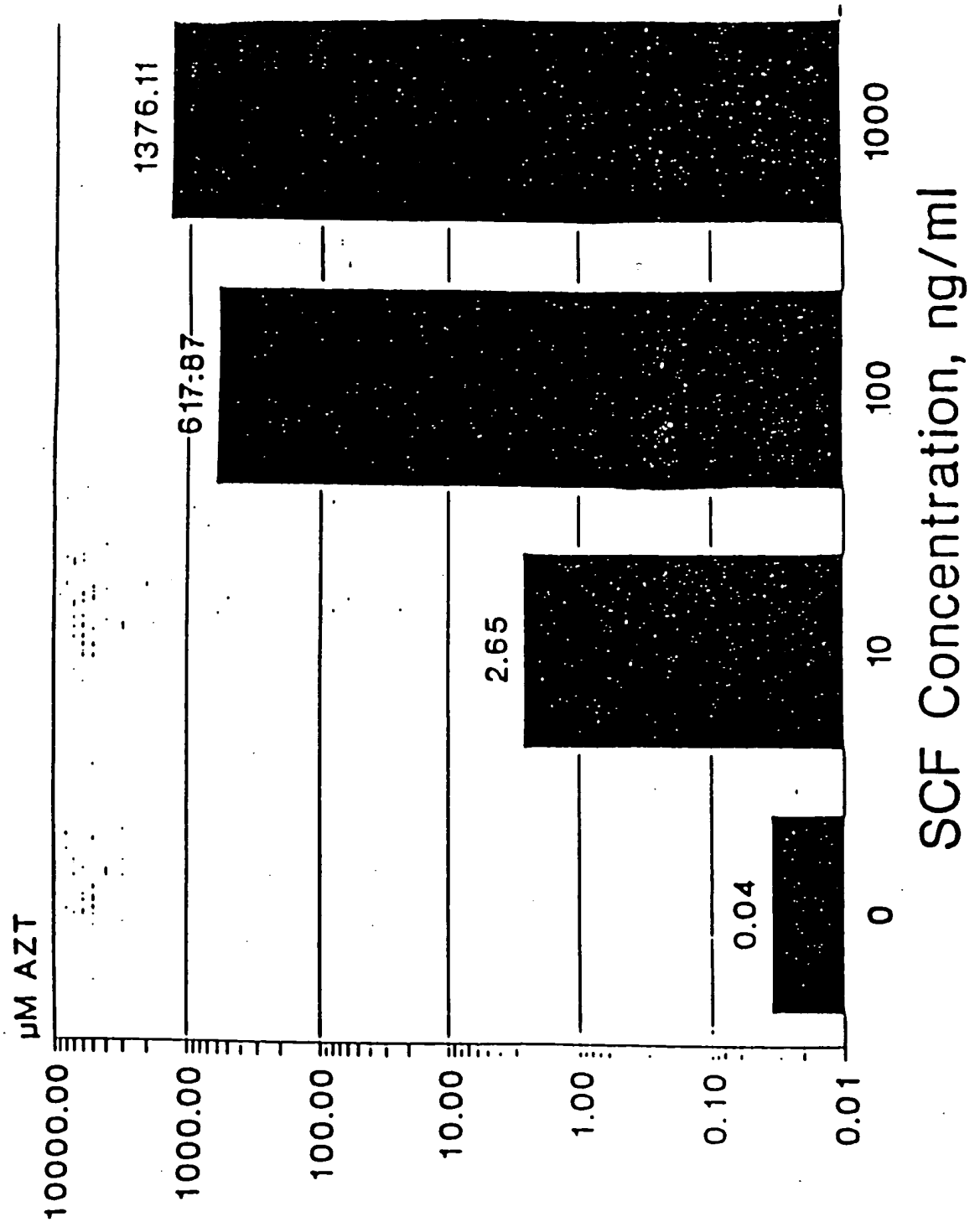


FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

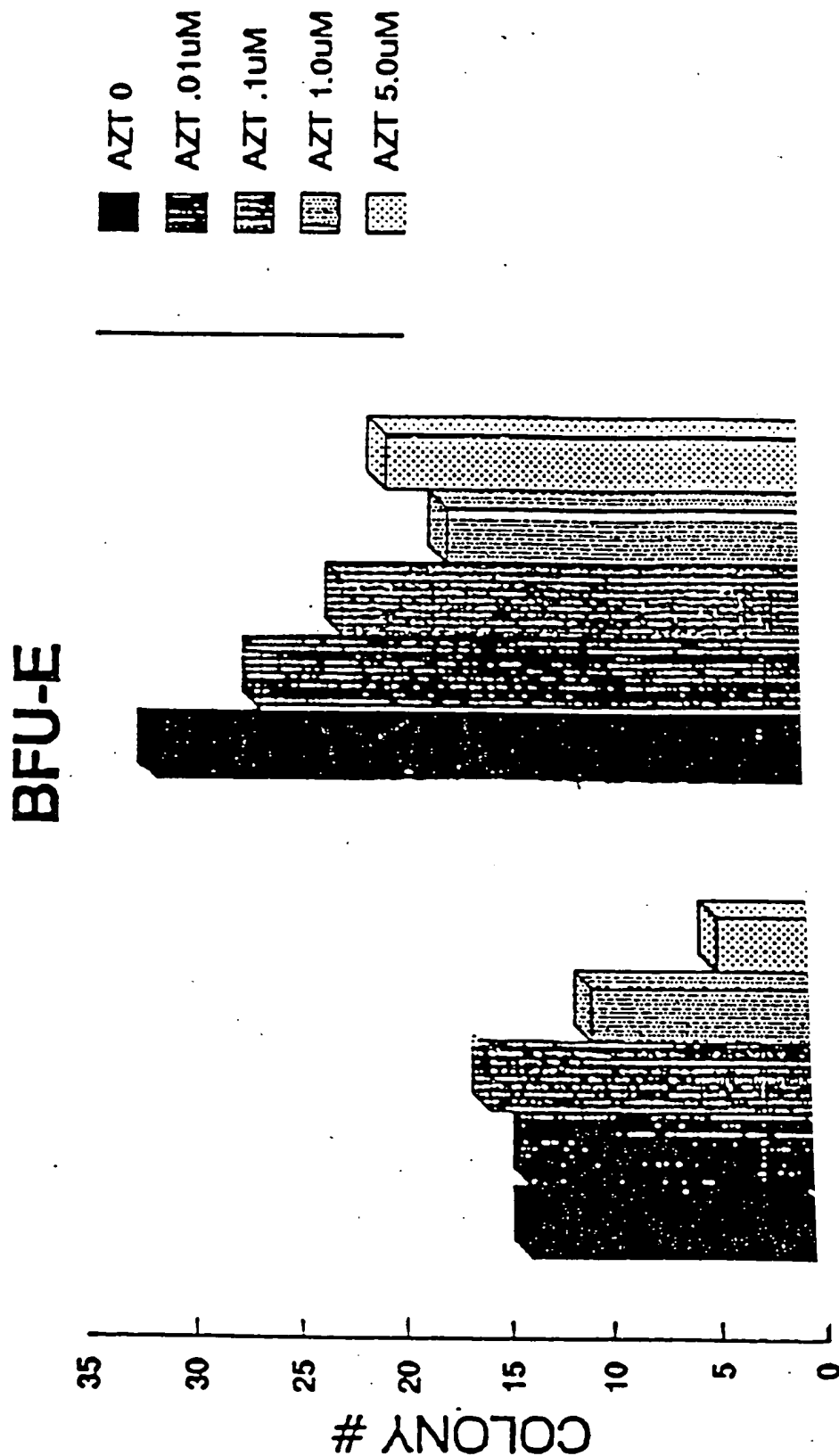


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

CFU-GM

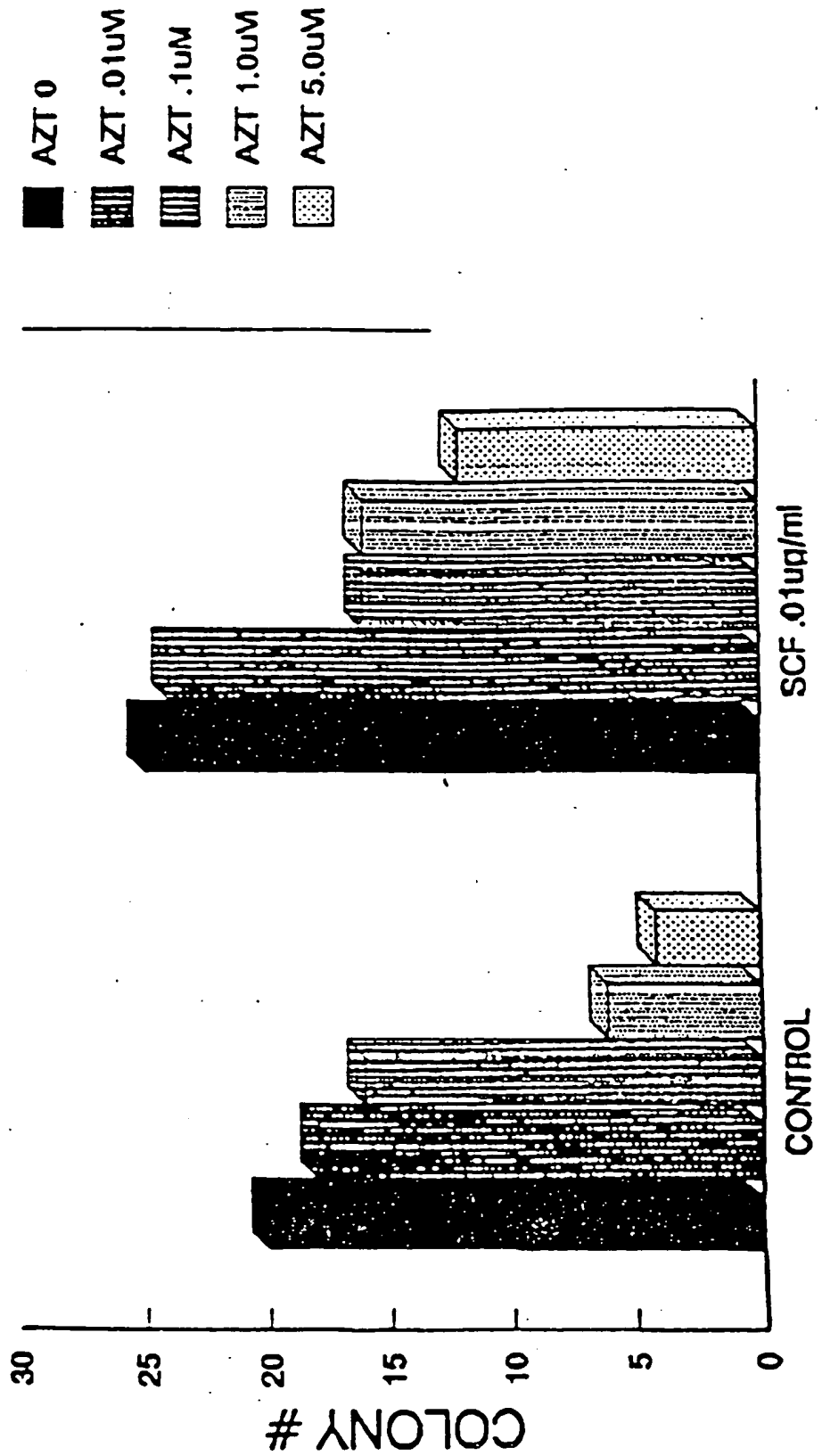
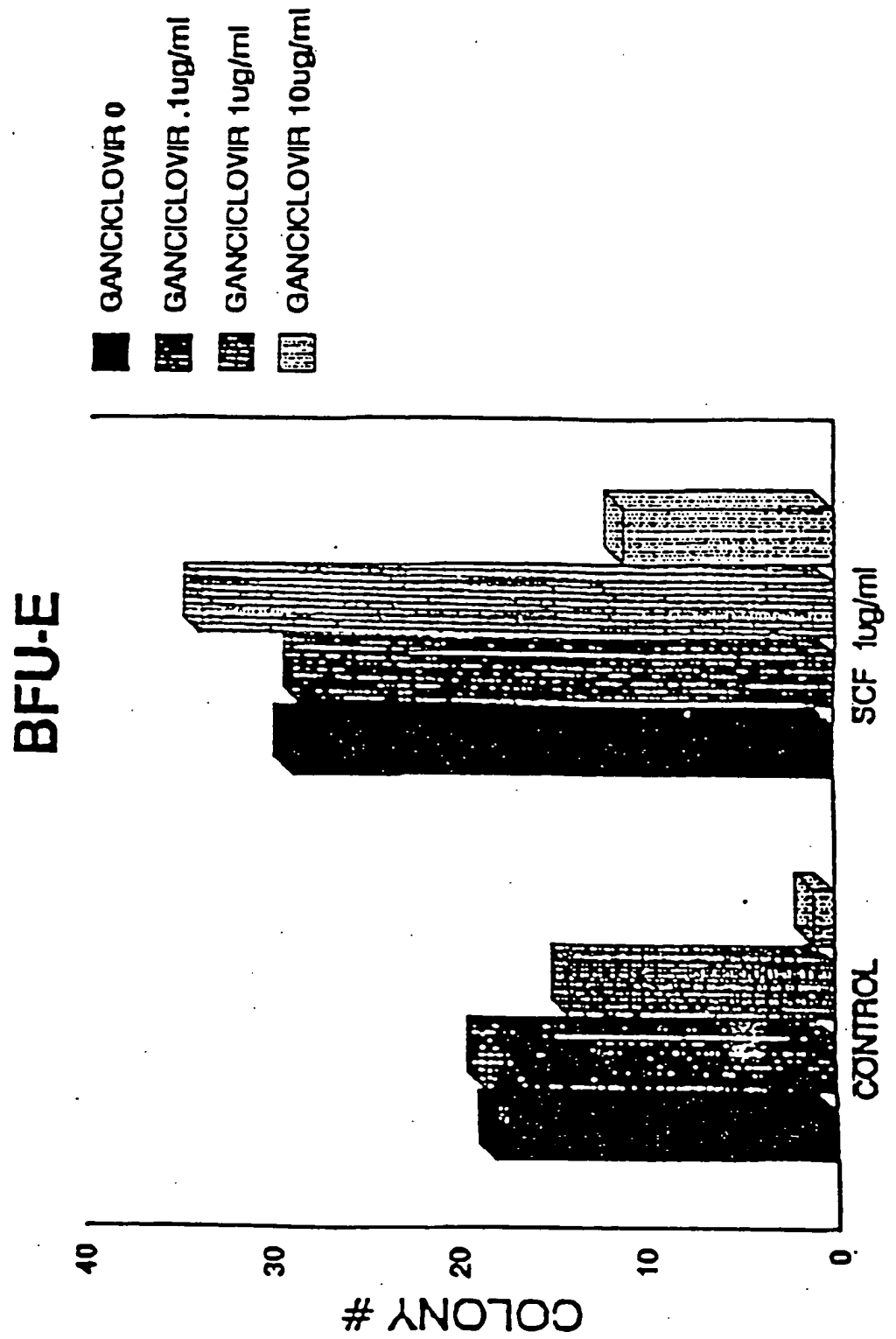


FIG. 64

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC



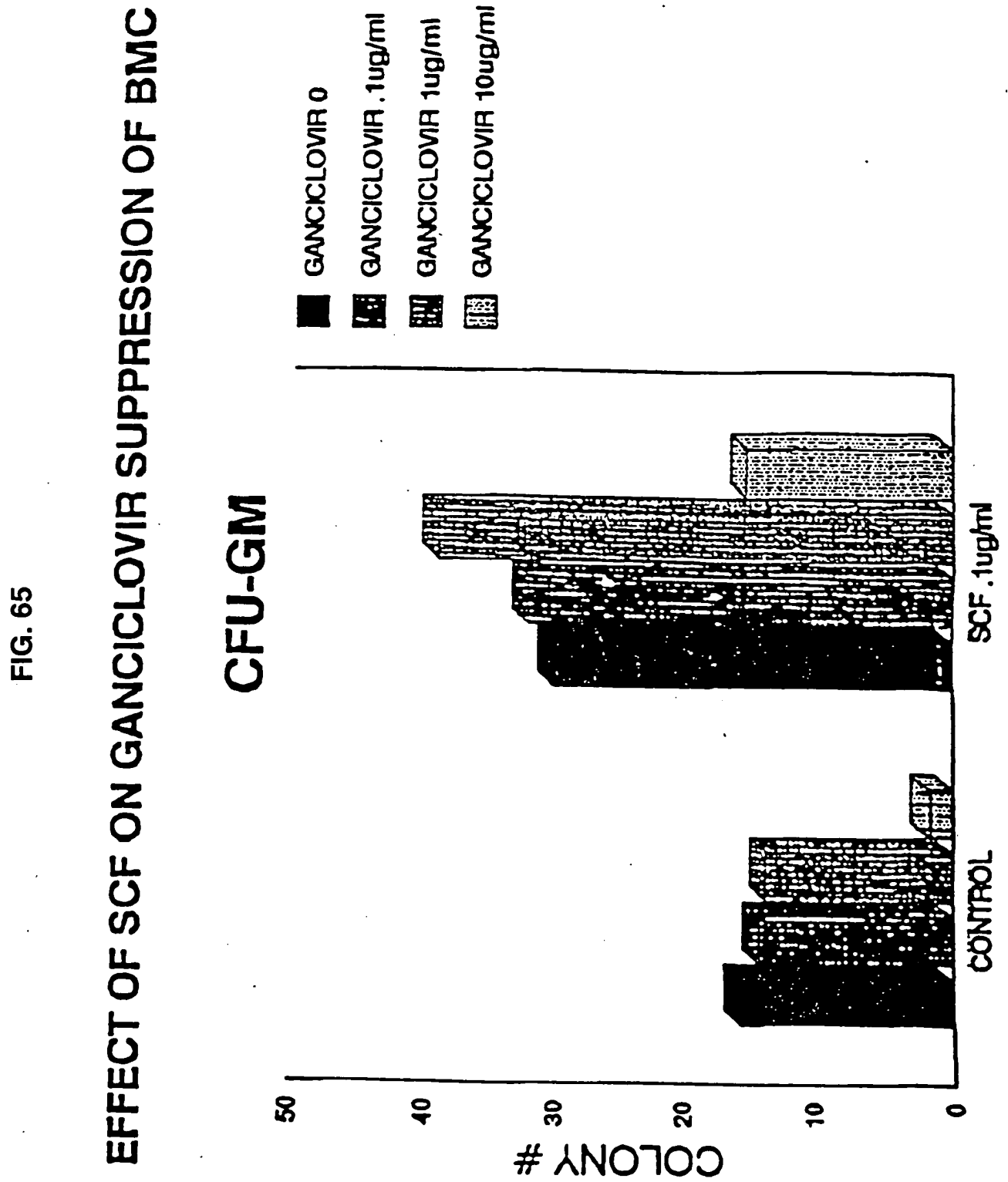


FIG. 66

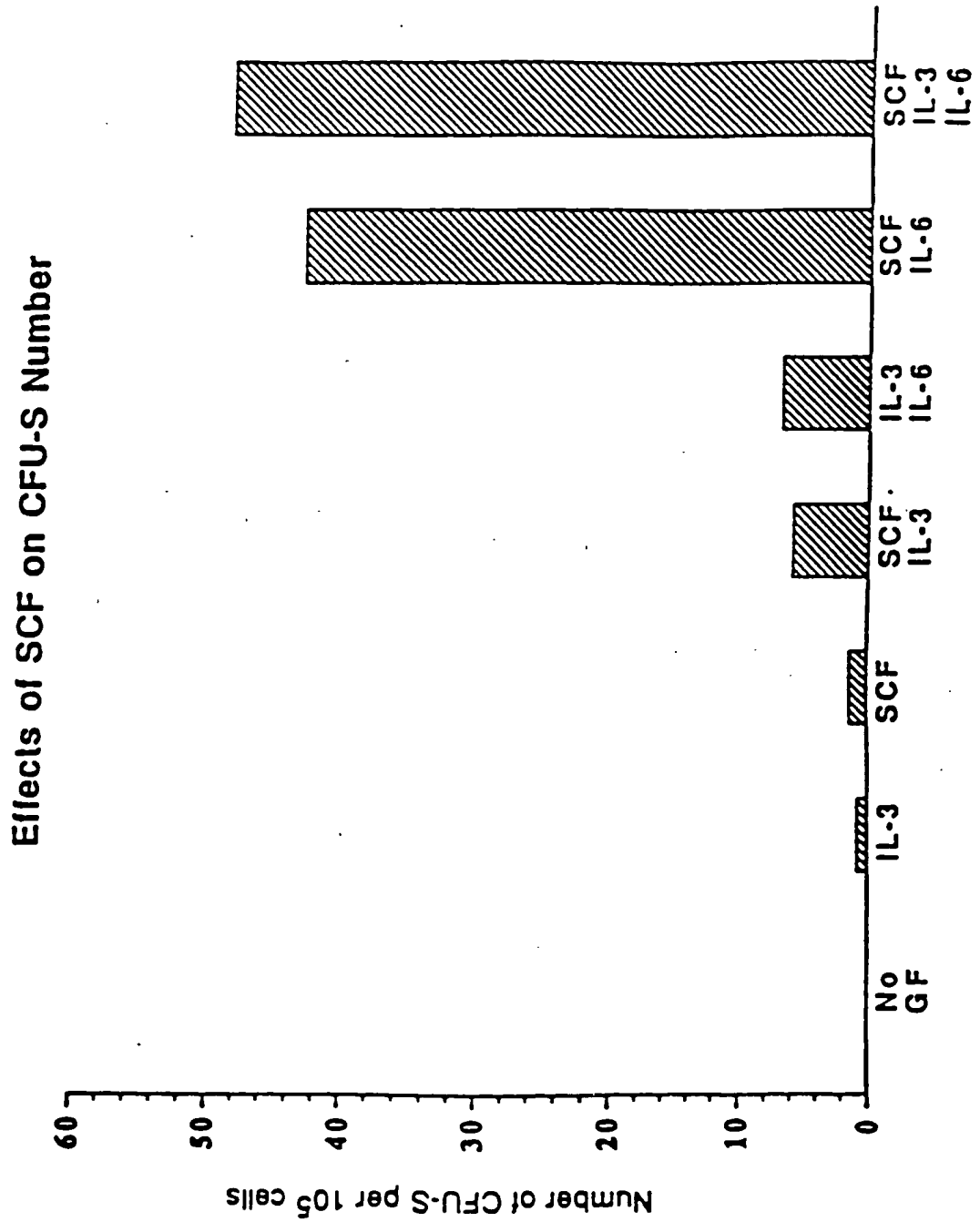


FIG. 67

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)

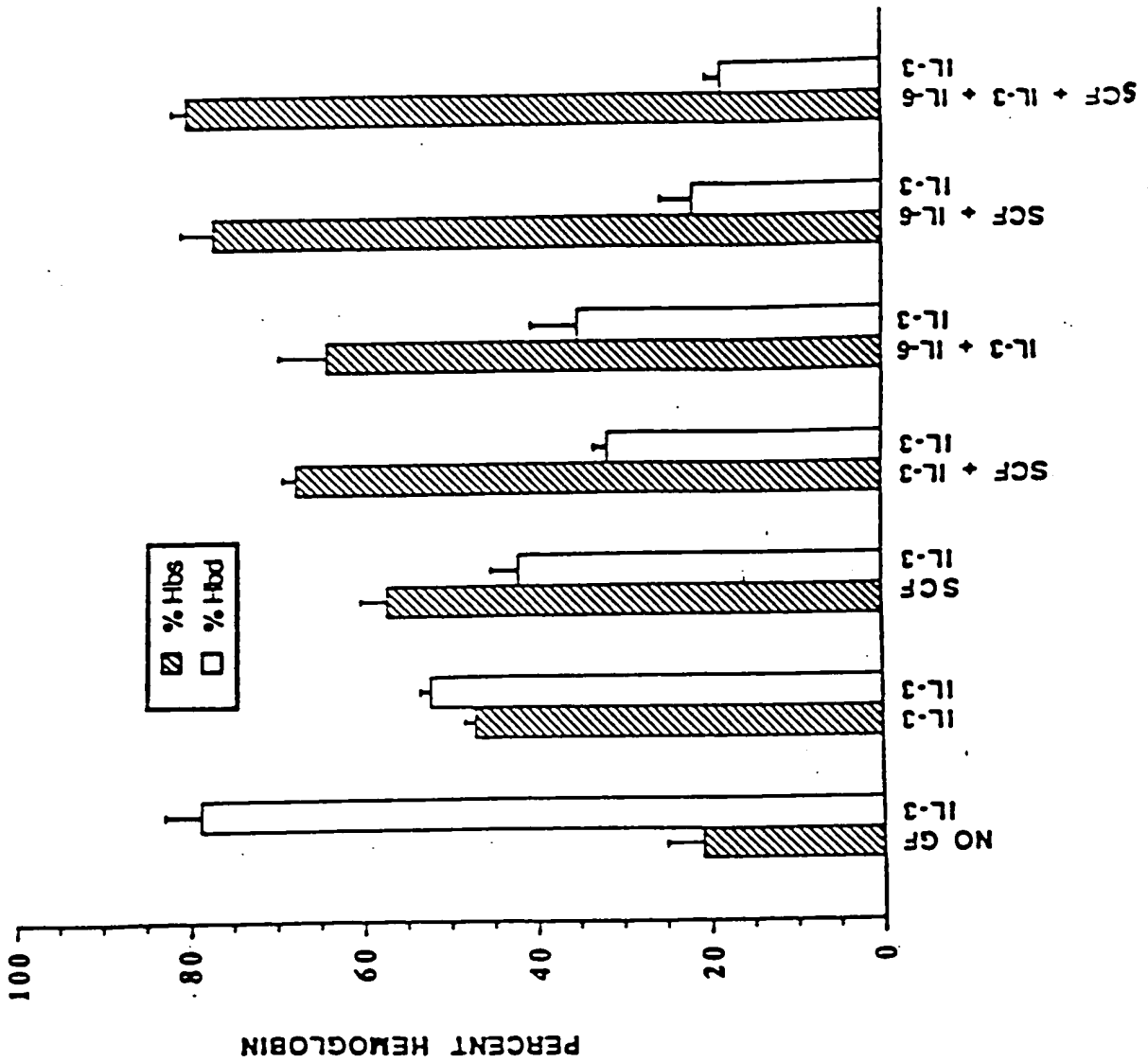


FIG. 68

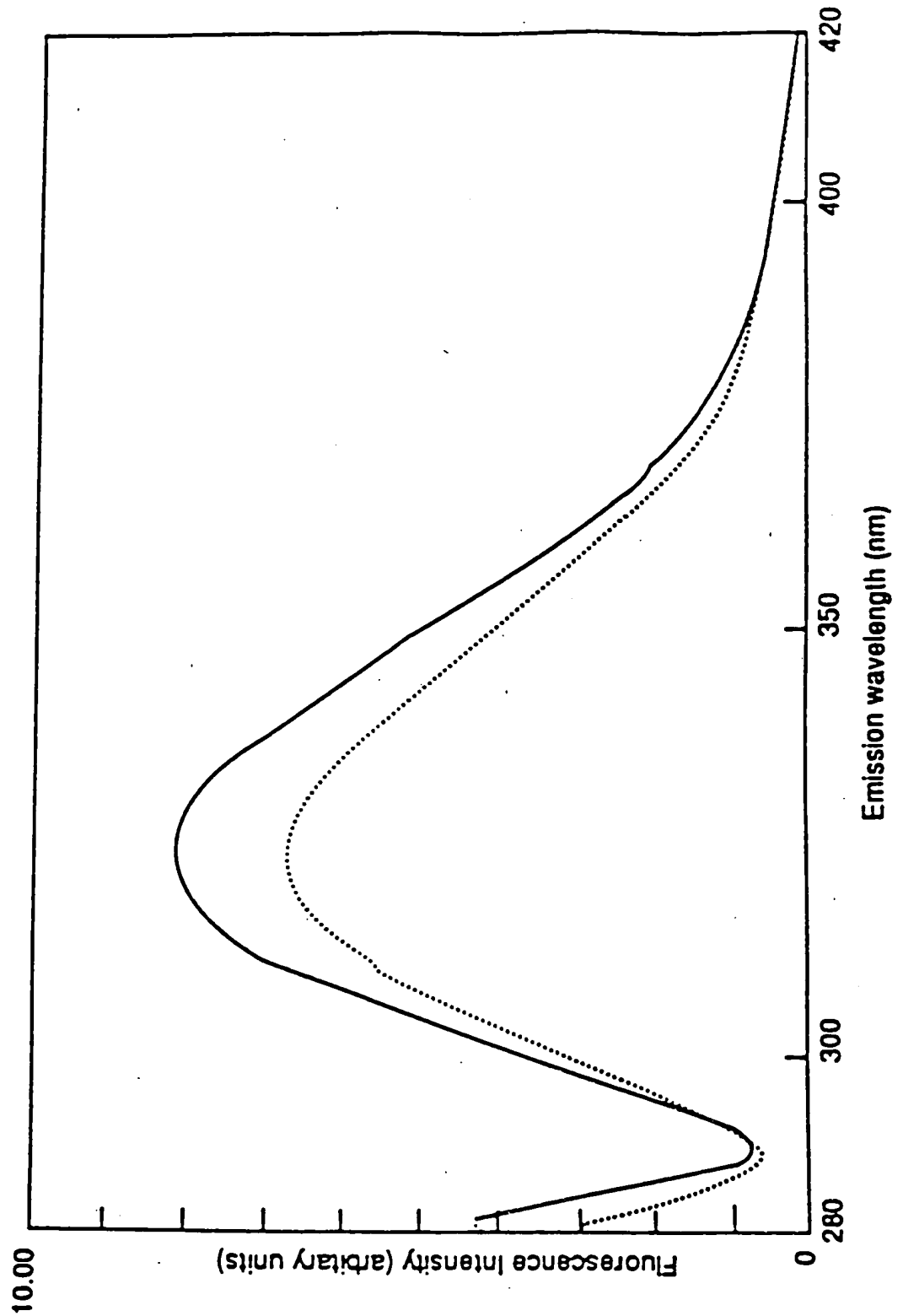


FIG. 69A

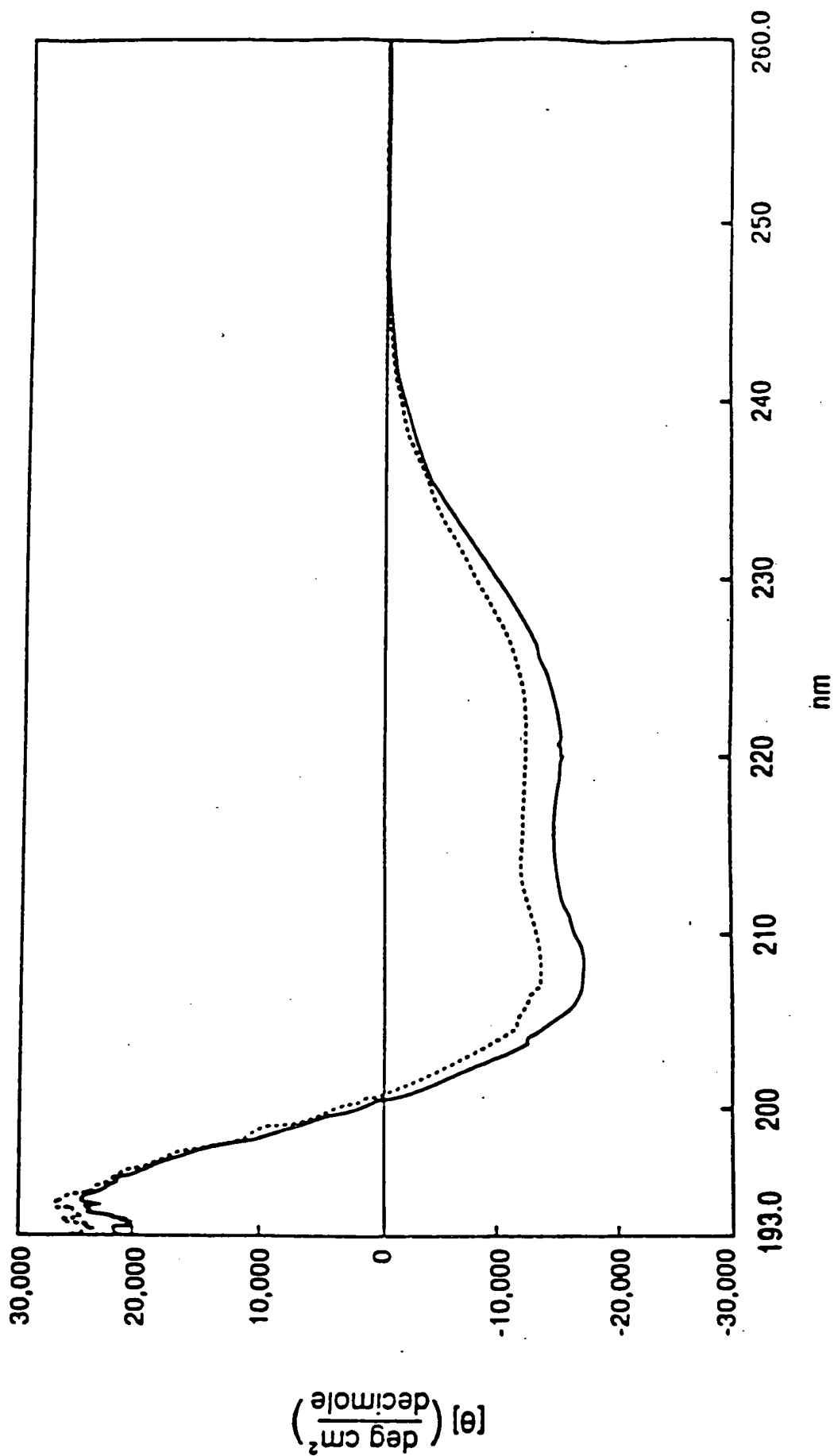


FIG. 69B

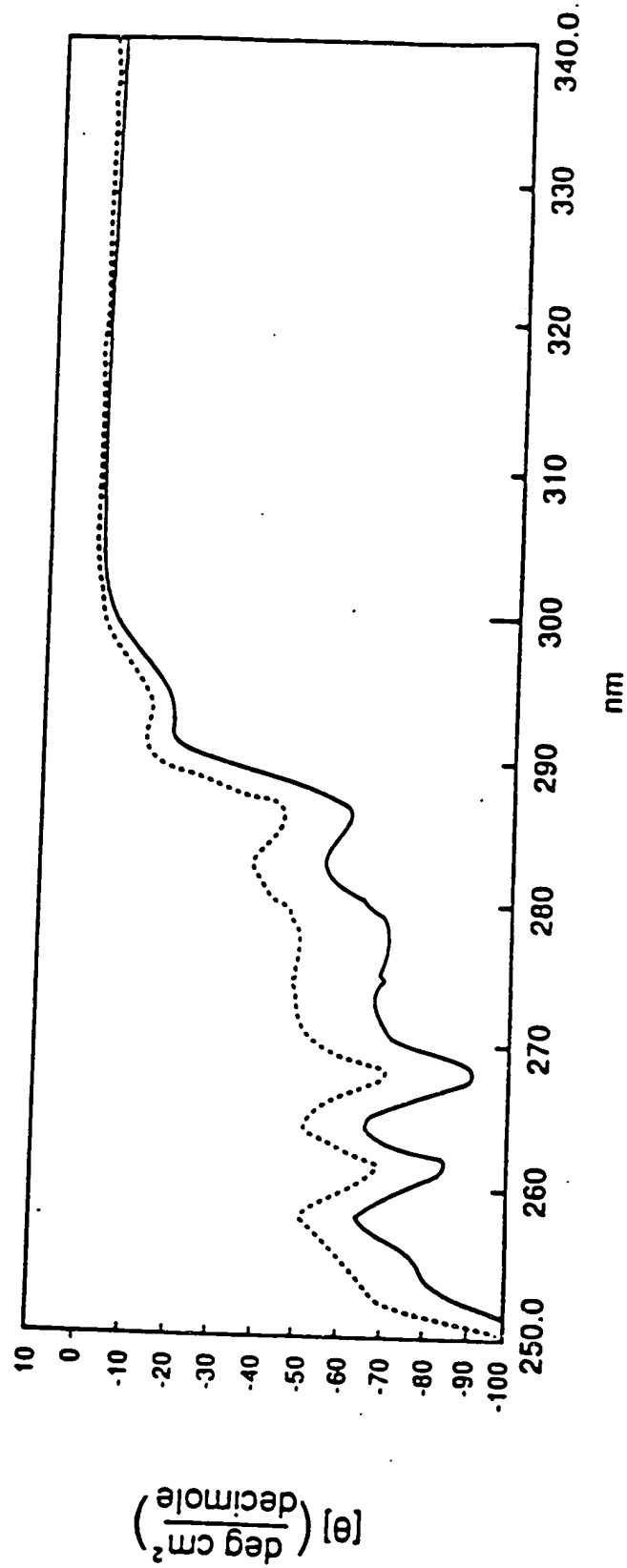


FIG. 70

